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## OM protein - protein search, using SW model

Run on: February 17, 2006, 02:44:17 ; Search time 47 Seconds

(without alignments)  
 17.591 Million cell updates/secTitle: US-10-734-049B-188  
 Perfect score: 56

Sequence: 1 LMAPPCHAL 10

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82765679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000000Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cggn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

2: /cggn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3: /cggn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4: /cggn2\_6/ptodata/1/iaa/PCRTUS\_COMB.pep:\*

5: /cggn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

6: /cggn2\_6/ptodata/1/iaa/backfilest.pep:\*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	%
1	56	100.0	312	2	US-09-230-637-34	Sequence 34, Appl	
2	56	100.0	313	2	US-09-34-878-30	Sequence 30, Appl	
3	56	100.0	313	2	US-09-367-007C-39	Sequence 39, Appl	
4	56	100.0	319	2	US-09-949-016-10160	Sequence 10160, A	
5	52	92.9	289	2	US-09-25-991A-31795	Sequence 31795, A	
6	51	91.1	337	2	US-08-75-669A-1	Sequence 1, Appl	
7	51	91.1	337	2	US-09-230-637-22	Sequence 22, Appl	
8	46	82.1	337	2	US-09-23-371A-1	Sequence 1, Appl	
9	48	85.7	290	2	US-09-230-637-32	Sequence 32, Appl	
10	48	85.7	301	2	US-09-230-637-33	Sequence 33, Appl	
11	47	83.9	612	2	US-09-20-895-3	Sequence 3, Appl	
12	46	82.1	322	2	US-09-13-001C-3194	Sequence 3194, Ap	
13	44	82.1	324	2	US-09-107-532A-6145	Sequence 6145, AP	
14	46	82.1	325	2	US-09-13-000C-4346	Sequence 4346, AP	
15	44	78.6	44	2	US-09-083-541-3	Sequence 3, Appl	
16	44	78.6	184	2	US-08-907-8000A-2	Sequence 2, Appl	
17	44	78.6	184	2	US-08-96-317-2	Sequence 2, Appl	
18	44	78.6	282	2	US-09-540-236-2576	Sequence 2576, AP	
19	44	78.6	286	2	US-09-328-352-8060	Sequence 8060, AP	
20	44	78.6	289	2	US-09-24-796A-18109	Sequence 18109, A	
21	44	78.6	294	2	US-09-230-637-31	Sequence 31, Appl	
22	43	76.8	161	2	US-09-905-540-14293	Sequence 14293, A	
23	40	71.4	118	2	US-09-48-039A-14244	Sequence 14244, A	
24	40	71.4	266	2	US-09-48-039A-10055	Sequence 10055, A	
25	39	69.6	351	2	US-09-61-912-8	Sequence 8, Appl	
26	37	66.1	170	1	US-08-47-451-12	Sequence 12, Appl	
27	36	64.3	102	2	US-09-955-392-20	Sequence 20, Appl	

28	111	US-09-087-031E-16	Sequence 16, Appl
29	111	US-10-014-055-5	Sequence 5, Appl
30	111	US-10-028-051A-5	Sequence 5, Appl
31	111	US-09-902-540-15035	Sequence 15035, A
32	111	US-08-255-74-C-76	Sequence 76, Appl
33	111	US-09-902-540-15709	Sequence 15709, A
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35	111	US-09-919-016-5953	Sequence 5953, AP
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36	111	US-09-534-638-5	Sequence 1, Appl
36	111	PCT-US93-03837-1	Sequence 10395, A
39	111	US-09-902-540-10395	Sequence 1, Appl
40	111	US-08-127-499A-1	Sequence 1, Appl
41	111	US-08-482-847-1	Sequence 1, Appl
42	111	US-10-360-101-162	Sequence 162, APP
43	111	US-09-534-638-5	Sequence 5, Appl
44	111	US-09-270-767-57195	Sequence 51195, A
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46	111	US-09-270-767-39225	Sequence 39225, A
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48	111	US-09-270-767-32903	Sequence 32903, A
49	111	US-09-270-767-48120	Sequence 48120, A
50	111	US-09-902-540-16237	Sequence 16237, A
51	111	US-09-252-991A-32256	Sequence 32756, A
52	111	US-09-252-991A-25655	Sequence 25695, A
53	111	US-09-538-092-17	Sequence 17, Appl
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55	111	US-09-910-009A-357	Sequence 357, APP
56	111	US-09-248-796A-21697	Sequence 21697, A
57	111	US-09-081-010-047-2358	Sequence 14, Appl
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59	111	US-09-917-067-13	Sequence 9, Appl
60	111	US-09-487-558B-248	Sequence 248, APP
61	111	US-09-833-737-110	Sequence 211, APP
62	111	US-09-311-731A-210	Sequence 210, APP
63	111	US-09-248-796A-22710	Sequence 22710, A
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66	111	US-09-538-092-887	Sequence 887, APP
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68	111	US-09-044-281-112	Sequence 211, APP
69	111	US-09-270-767-34646	Sequence 24646, A
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76	111	US-09-270-767-52993	Sequence 23, Appl
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82	111	US-09-635-521-52	Sequence 7618, AP
83	111	US-09-224-683-52	Sequence 18031, A
84	111	US-09-604-325A-52	Sequence 59, APP
85	111	US-09-232-991A-17447	Sequence 36, Appl
86	111	US-08-316-728A-52	Sequence 2, Appl
87	111	US-08-311-731A-89	Sequence 100, APP
88	111	US-09-358-352-5814	Sequence 7012, AP
89	111	US-09-949-016-7618	Sequence 9825, AP
90	111	US-09-604-325A-52	Sequence 59, APP
91	111	US-09-538-092-594	Sequence 36, Appl
92	111	US-09-327-984A-36	Sequence 2, Appl
93	111	US-10-243-789-2	Sequence 100, APP
94	111	US-09-83-731-100	Sequence 7012, AP
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97	111	US-09-228-984A-72	Sequence 72, APP
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249	31	55.4	234	2	US-09-252-991A-29027	Sequence 29027, A	Patent No. 5,96516.
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273	31	55.4	367	2	US-08-780-311A-2	Sequence 2, ADP	Sequence 9, Appli
274	31	55.4	368	2	US-09-614-912-4	Sequence 4, ADP	Sequence 3, ADP
275	31	55.4	383	2	US-09-94-16-9989	Sequence 9989, AD	Sequence 7, ADP
276	31	55.4	393	2	US-09-252-991A-23796	Sequence 23796, A	Sequence 15, ADP
277	31	55.4	399	2	US-09-252-991A-16821	Sequence 16821, A	Sequence 15, ADP
278	31	55.4	402	1	US-08-460-06-11	Sequence 11, ADP	Sequence 11, ADP
279	31	55.4	402	1	US-08-325-630-11	Sequence 11, ADP	Sequence 11, ADP
280	31	55.4	408	2	US-09-252-991A-19312	Sequence 19312, A	Sequence 14, ADP
281	31	55.4	412	2	US-09-743-742B-8	Sequence 8, ADP	Sequence 9, ADP
282	31	55.4	421	2	US-09-949-016-11670	Sequence 11670, A	Sequence 11, ADP
283	31	55.4	452	2	US-09-902-540-9902	Sequence 9002, AD	Sequence 11, ADP
284	31	55.4	467	2	US-10-104-047-2838	Sequence 2838, AD	Sequence 11, ADP
285	31	55.4	489	1	US-08-895-521-1	Sequence 1, ADP	Sequence 1, ADP
286	31	55.4	489	1	US-08-895-521-3	Sequence 3, ADP	Sequence 3, ADP
287	31	55.4	489	2	US-09-235-218-1	Sequence 1, ADP	Sequence 1, ADP
288	31	55.4	489	2	US-09-235-218-3	Sequence 3, ADP	Sequence 1, ADP
289	31	55.4	542	2	US-09-248-796A-27163	Sequence 27163, A	Sequence 4, ADP
290	31	55.4	560	2	US-09-902-25999	Sequence 25999, A	PCT-US94-08063-1
291	31	55.4	603	1	US-08-190-802A-50	Sequence 50, ADP	Sequence 5365, ADP
292	31	55.4	603	2	US-08-767-346-50	Sequence 50, ADP	Sequence 5365, ADP
293	31	55.4	603	2	US-08-473-089-50	Sequence 50, ADP	Sequence 5366, ADP
294	31	55.4	603	2	US-08-48-072A-50	Sequence 50, ADP	Sequence 53662, ADP
295	31	55.4	619	2	US-09-443-067-20	Sequence 20, ADP	Sequence 5079, A
296	31	55.4	642	1	US-08-705-936-2	Sequence 2, ADP	Sequence 11961, ADP
297	31	55.4	643	1	US-08-616-844-39	Sequence 39, ADP	Sequence 457, ADP
298	31	55.4	643	1	US-08-599-654-39	Sequence 439, ADP	Sequence 6, ADP
299	31	55.4	643	2	US-08-944-868A-39	Sequence 39, ADP	Sequence 62, ADP
300	31	55.4	643	2	US-08-944-423A-39	Sequence 39, ADP	Sequence 1, ADP
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303	31	55.4	643	2	US-09-949-016-6645	Sequence 6645, ADP	Sequence 52, ADP
304	31	55.4	653	2	US-09-198-452A-439	Sequence 439, ADP	Sequence 92, ADP
305	31	55.4	674	2	US-09-949-016-8912	Sequence 421, ADP	Sequence 21137, A
306	31	55.4	676	2	US-09-438-185A-421	Sequence 2, ADP	Sequence 58, ADP
307	31	55.4	676	2	US-09-764-246-2	Sequence 6027, ADP	Sequence 54, ADP
308	31	55.4	677	2	US-09-057-081B-28	Sequence 4, ADP	Sequence 2446, ADP
309	31	55.4	677	2	US-09-949-016-6645	Sequence 4, ADP	Sequence 18, ADP
310	31	55.4	677	2	US-09-198-452A-439	Sequence 439, ADP	Sequence 6, ADP
311	31	55.4	679	2	US-09-949-016-8912	Sequence 421, ADP	Sequence 58, ADP
312	31	55.4	712	2	US-09-252-991A-20471	Sequence 20471, A	Sequence 34199, A
313	31	55.4	747	2	US-09-764-246-2	Sequence 6027, ADP	Sequence 4916, A
314	31	55.4	747	2	US-10-020-445A-459	Sequence 459, ADP	Sequence 48, ADP
315	31	55.4	757	2	US-09-902-540-9952	Sequence 9952, ADP	Sequence 41921, A
316	31	55.4	858	1	US-09-252-991A-17399	Sequence 17399, A	Sequence 10680, A
317	31	55.4	913	1	US-08-220-151-6	Sequence 6, ADP	Sequence 21605, A
318	31	55.4	913	1	US-08-413-118-6	Sequence 6, ADP	Sequence 6421, ADP
319	31	55.4	913	2	US-08-473-446-6	Sequence 6, ADP	Sequence 32025, A

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394	53.6	203	2	US-09-252-991A-30744	Sequence 30744, A	Sequence 27508, A
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396	53.6	208	2	US-09-449-249-8	Sequence 8, Appli	Sequence 8, Appli
397	53.6	224	2	US-10-104-047-2601	Sequence 2601, Ap	Sequence 29215, A
398	53.6	229	2	US-09-540-236-3625	Sequence 3625, Ap	Sequence 2, Appli
399	53.6	235	2	US-09-160-699-2	Sequence 2, Appli	Sequence 2, Appli
400	53.6	235	2	US-10-188-947-3	Sequence 3, Appli	Sequence 2, Appli
401	53.6	249	2	US-09-540-14388	Sequence 14988, A	Sequence 174, App
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403	53.6	259	2	US-09-255-991A-22293	Sequence 23293, A	Sequence 12, Appli
404	53.6	269	2	US-09-270-767-45287	Sequence 45287, A	Sequence 12, Appli
405	53.6	270	2	US-09-205-228-568	Sequence 568, APP	Sequence 12, Appli
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419	53.6	311	2	US-09-252-991A-18916	Sequence 10107, A	Sequence 431, APP
420	53.6	316	2	US-09-302-540-10107	Sequence 1, Appli	Sequence 431, APP
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426	53.6	369	4	PCT-US94-02991-69	Sequence 69, Appli	Sequence 452, APP
427	53.6	372	2	US-09-889-039A-7198	Sequence 7398, AP	Sequence 750, APP
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430	53.6	392	2	US-09-128-532-5819	Sequence 5819, AP	Sequence 6193, AP
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435	53.6	423	1	US-09-808-641-1	Sequence 1, Appli	Sequence 452, AP
436	53.6	423	2	US-09-054-839-1	Sequence 1, Appli	Sequence 452, AP
437	53.6	427	2	US-09-551-438-1	Sequence 1, Appli	Sequence 452, AP
438	53.6	444	2	US-09-252-991A-30420	Sequence 30420, A	Sequence 452, AP
439	53.6	448	2	US-09-149-016-9960	Sequence 9960, AP	Sequence 452, AP
440	53.6	454	2	US-09-252-991A-25907	Sequence 25907, A	Sequence 452, AP
441	53.6	459	2	US-09-152-991A-22601	Sequence 22601, A	Sequence 452, AP
442	53.6	467	2	US-09-151-438-1	Sequence 23045, A	Sequence 452, AP
443	53.6	521	2	US-09-252-991A-30311	Sequence 30311, A	Sequence 452, AP
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445	53.6	600	2	US-09-252-991A-16741	Sequence 16741, A	Sequence 452, AP
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448	53.6	680	1	US-08-211-430-2	Sequence 2, Appli	Sequence 452, AP
449	53.6	690	2	US-09-261-136-1	Sequence 1, Appli	Sequence 452, AP
450	53.6	680	2	US-09-516-967-1	Sequence 2, Appli	Sequence 452, AP
451	53.6	680	2	US-10-219-541-1	Sequence 1, Appli	Sequence 452, AP
452	53.6	686	2	US-09-173-151A-4	Sequence 4, Appli	Sequence 452, AP
453	53.6	690	2	US-09-291-170A-2	Sequence 2, Appli	Sequence 452, AP
454	53.6	690	2	US-09-724-884-2	Sequence 2, Appli	Sequence 452, AP
455	53.6	690	2	US-09-224-532-2	Sequence 2, Appli	Sequence 452, AP
456	53.6	690	2	US-09-673-222-2	Sequence 2, Appli	Sequence 452, AP
457	53.6	701	2	US-09-087-727-2	Sequence 2, Appli	Sequence 452, AP
458	53.6	701	2	US-09-853-053-2	Sequence 2, Appli	Sequence 452, AP
459	53.6	701	2	US-09-949-016-6026	Sequence 6026, AP	Sequence 452, AP
460	53.6	763	1	US-08-677-862-2	Sequence 2, Appli	Sequence 452, AP
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463	53.6	763	2	US-08-789-275-4	Sequence 4, Appli	Sequence 452, AP
464	53.6	763	2	US-09-949-016-902	Sequence 5, Appli	Sequence 452, AP
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543	29	51.8	163	2	US-09-270-767-1738	Sequence 3138, A
544	29	51.8	163	2	US-09-270-767-46955	Sequence 46955, A
545	29	51.8	168	2	US-09-252-991A-27144	Sequence 27144, A
546	29	51.8	178	2	US-09-489-039A-10475	Sequence 10475, A
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548	29	51.8	188	2	US-09-270-767-51217	Sequence 51217, A
549	29	51.8	192	2	US-09-198-452A-830	Sequence 830, App
550	29	51.8	194	2	US-09-248-796A-24122	Sequence 24122, A
551	29	51.8	197	2	US-09-328-352-7839	Sequence 7839, AP
552	29	51.8	200	2	US-09-710-279-394	Sequence 394, A
553	29	51.8	200	2	US-09-710-279-1242	Sequence 1242, AP
554	29	51.8	202	2	US-09-480-297A-8	Sequence 8, Appli
555	29	51.8	202	2	US-09-74-74-259-8	Sequence 8, Appli
556	29	51.8	202	2	US-09-816-6-44-8	Sequence 8, Appli
557	29	51.8	206	2	US-09-134-001C-39299	Sequence 39299, AP
558	29	51.8	207	2	US-09-252-991A-3113	Sequence 32113, A
559	29	51.8	208	2	US-09-902-540-16427	Sequence 16427, A
560	29	51.8	211	2	US-09-270-767-42667	Sequence 42667, A
561	29	51.8	218	2	US-09-438-115A-783	Sequence 783, App
562	29	51.8	219	2	US-09-902-540-14094	Sequence 14094, A
563	29	51.8	220	2	US-09-252-991A-28993	Sequence 28993, A
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573	29	51.8	231	4	PCT-US95-03866-6	Sequence 6, Appli
574	29	51.8	233	2	US-10-305-770B-2	Sequence 2, Appli
575	29	51.8	234	2	US-09-252-991A-322510	Sequence 322510, A
576	29	51.8	236	2	US-09-489-039A-83755	Sequence 83755, AP
577	29	51.8	252	2	US-08-812-586-48	Sequence 48, Appli
578	29	51.8	252	2	US-09-533-832A-45	Sequence 45, Appli
579	29	51.8	256	1	US-09-993-960-3	Sequence 3, Appli
580	29	51.8	256	2	US-09-368-240-3	Sequence 3, Appli
581	29	51.8	256	2	US-09-468-702-3	Sequence 3, Appli
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583	29	51.8	258	2	US-09-543-681A-7629	Sequence 7629, AP
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586	29	51.8	279	2	US-09-368-240-1	Sequence 1, Appli
587	29	51.8	279	2	US-09-468-702-1	Sequence 1, Appli
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589	29	51.8	287	2	US-09-503-097A-25	Sequence 25, Appli
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591	29	51.8	311	2	US-09-543-681A-5603	Sequence 5603, AP
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593	29	51.8	315	2	US-09-270-767-46735	Sequence 46735, A
594	29	51.8	320	2	US-10-104-047-2641	Sequence 2641, AP
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596	29	51.8	339	2	US-09-252-991A-28087	Sequence 28087, A
597	29	51.8	350	2	US-09-252-991A-28377	Sequence 28377, A
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602	29	51.8	351	2	US-09-430-775-32	Sequence 32, Appli
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608	29	51.8	369	1	US-08-595-974-4	Sequence 6187, AP
609	29	51.8	369	2	US-09-195-786-2	Sequence 819, AP
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51.8	29	51.8	375	4	PCT-US94-14436-28	Sequence 28, APPL
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51.8	29	51.8	451	2	US-09-252-991A-29903	Sequence 860, APP
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51.8	29	51.8	492	2	US-10-113-794A-2	Sequence 12, APPL
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51.8	29	51.8	514	2	US-09-715-594-314	Sequence 11511, A
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51.8	29	51.8	519	2	US-09-538-092-1292	Sequence 26, APPL
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51.8	29	51.8	520	2	US-09-175-928-4	Sequence 2, APPL
51.8	29	51.8	538	2	US-09-949-016-1511	Sequence 515, APPL
51.8	29	51.8	540	2	US-09-715-594-26	Sequence 515, APPL
51.8	29	51.8	540	2	US-09-902-14087	Sequence 14087, A
51.8	29	51.8	557	2	US-09-902-14087	Sequence 994, APP
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972	28	US-08-384-616-38	Sequence 38, Appl	2
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974	28	US-09-315-850-38	Sequence 38, Appl	2
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976	28	US-09-854-864-10	Sequence 10, Appl	2



NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 10160  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Human  
US-09-349-016-10160

Query Match 100.0%; Score 56; DB 2; Length 339;  
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Number of Sequences: 20

Qy 1 LMLAPPCHL 10  
Db 215 LMLAPPCHL 224

RESULT 5  
US-09-252-991A-31795  
; Sequence 31795, Application US/09252991A  
; Patent No. 6551795

GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfeld et al.  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDONOMAS

FILE FILING DATE: 1998-02-18  
PRIORITY NUMBER: US 60/094,190  
PRIORITY APPLICATION NUMBER: US 60/094,190  
PRIORITY FILING DATE: 1998-02-18  
NUMBER OF SEQ ID NOS: 33142

CURRENT APPLICATION NUMBER: US/09/252,391A  
PRIORITY NUMBER: US 60/074,788  
PRIORITY APPLICATION NUMBER: US 60/094,190  
PRIORITY FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

Query Match 92.9%; Score 52; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.64; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Number of Sequences: 20

Qy 2 LMLAPPCHL 10  
Db 166 LMLAPPCHL 174

RESULT 6  
US-08-757-669A-1  
; Sequence 1, Application US/08757669A  
; Patent No. 6183751

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; APPLICANT: Russo, James J.  
; APPLICANT: Edelman, Isidore S.  
; APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS  
TITLE OF INVENTION: SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSSEEB: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
ZIP: 10036

COMPUTER READABLE FORM:  
; COMPUTER TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,669A  
; FILING DATE: 1998-07-27  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
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; REFERENCE/DOCKET NUMBER: 451.85-F  
; TELECOMMUNICATION INFORMATION:  
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; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 337 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-757-669A-1

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Best Local Similarity 90.0%; Pred. No. 1.1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMLAPPCHL 10  
Db 213 LMLAPPCHL 222

RESULT 7  
US-09-230-637-22  
; Sequence 22, Application US/09230637  
; Patent No. 6264958

GENERAL INFORMATION:  
; APPLICANT: Hayward, Gary  
; APPLICANT: Nicholas, John  
; APPLICANT: Hardwick, J. Marie  
; APPLICANT: Reitz, Marvin  
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma  
; TITLE OF INVENTION: Associated Herpesvirus  
; FILE REFERENCE: 1107-78372  
; CURRENT APPLICATION NUMBER: US/09/230,637  
; CURRENT FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/022,591  
; PRIOR FILING DATE: 1996-07-25  
; PRIOR APPLICATION NUMBER: PCT US 97/12931  
; PRIOR FILING DATE: 1997-07-24  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 22

LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Kaposi's sarcoma-associated herpes-like virus  
US-09-230-637-22

Query Match 91.1%; Score 51; DB 2; Length 337;  
Best Local Similarity 90.0%; Pred. No. 1.1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMLAPPCHL 10  
Db 213 LMLAPPCHL 222

RESULT 8  
US-09-230-371A-1  
; Sequence 1, Application US/09230371A  
; Patent No. 6348586

GENERAL INFORMATION:  
; APPLICANT: Chang, Yuan  
; APPLICANT: Bohenzky, Roy A.  
; APPLICANT: Russo, James J.  
; APPLICANT: Edelman, Isidore S.  
; APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS  
TITLE OF INVENTION: SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSSEEB: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
ZIP: 10036

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND USES THEREOF  
 TITLE OF INVENTION: USBS THEREOF  
 FILE REFERENCE: 45185-G-PCT-US  
 CURRENT APPLICATION NUMBER: US/09/230,371A  
 CURRENT FILING DATE: 1999-11-17  
 PRIOR APPLICATION NUMBER: PCT/US97/13346  
 PRIOR FILING DATE: 1997-07-22  
 NUMBER OF SEQ ID NOS: 30  
 SEQ ID NO: 1  
 LENGTH: 337  
 TYPE: PRT  
 ORGANISM: Kaposi's sarcoma-associated herpesvirus  
 US-09-230-371A-1

Query Match Score 51; DB 2; Length 337;  
 Best Local Similarity 90.0%; Pred. No. 1.1;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 213 LMALPPCHLL 222

---

RESULT 9  
 US-09-230-637-32  
 Sequence 32, Application US/09230637  
 Patent No. 6264958  
 GENERAL INFORMATION:  
 APPLICANT: Hayward, Gary  
 APPLICANT: Nicholas, John  
 APPLICANT: Hardwick, J. Marie  
 APPLICANT: Reitz, Marvin  
 TITLE OF INVENTION: No. 6264958<1> Genes of Kaposi's Sarcoma  
 CURRENT APPLICATION NUMBER: US/09/230,637  
 CURRENT FILING DATE: 1999-11-23  
 FILE REFERENCE: 11.07-78372  
 PRIOR APPLICATION NUMBER: 60/022,591  
 PRIOR FILING DATE: 1996-07-25  
 PRIOR APPLICATION NUMBER: PCT US 97/12931  
 PRIOR FILING DATE: 1997-07-24  
 NUMBER OF SEQ ID NOS: 62  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 32  
 LENGTH: 290  
 TYPE: PRT  
 ORGANISM: H. atelies  
 US-09-230-637-32

Query Match Score 48; DB 2; Length 290;  
 Best Local Similarity 88.9%; Pred. No. 2.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 167 MALPPCHLL 175

---

RESULT 10  
 US-09-230-637-33  
 Sequence 33, Application US/09230637  
 Patent No. 6264958  
 GENERAL INFORMATION:  
 APPLICANT: Hayward, Gary  
 APPLICANT: Nicholas, John  
 APPLICANT: Hardwick, J. Marie  
 APPLICANT: Reitz, Marvin  
 TITLE OF INVENTION: No. 6264958<1> Genes of Kaposi's Sarcoma  
 CURRENT APPLICATION NUMBER: US/09/230,637  
 CURRENT FILING DATE: 1999-11-23  
 FILE REFERENCE: GTC-007  
 PRIOR APPLICATION NUMBER: US/09/134,001C  
 PRIOR FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/064,964  
 PRIOR FILING DATE: 1997-11-08  
 PRIOR APPLICATION NUMBER: US 60/055,779  
 PRIOR FILING DATE: 1997-08-14  
 NUMBER OF SEQ ID NOS: 5674  
 SEQ ID NO 3194  
 LENGTH: 322

TYPE: PRT  
 ORGANISM: *Staphylococcus epidermidis*  
 US-09-134-001C-194

Query Match Score 46; DB 2; Length 322;  
 Best Local Similarity 77.8%; Pred. No. 6.3%;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 200 MALPPCHTM 208

RESULT 13  
 US-09-107-5322A-6145  
 Sequence 6145, Application US/09107532A  
 Patent No. 6583275

GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO  
*ENTEROCOCCUS FAECIUM* FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02454

COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6145:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 324 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: *Enterococcus faecium*

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (B) LOCATION 1...324

SEQUENCE DESCRIPTION: SEQ ID NO: 6145;  
 US-09-107-5322A-6145

Query Match Score 46; DB 2; Length 324;  
 Best Local Similarity 77.8%; Pred. No. 6.4%;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 201 MALPPCHTM 209

RESULT 14  
 US-09-134-000C-4346  
 Sequence 4346, Application US/09134000C  
 Patent No. 6617156

GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO  
*ENTEROCOCCUS FAECALIS* FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 CURRENT FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/055,778  
 PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 4346  
 LENGTH: 325

TYPE: PRT  
 ORGANISM: *Enterococcus faecalis*  
 US-09-134-000C-4346

Query Match Score 46; DB 2; Length 325;  
 Best Local Similarity 77.8%; Pred. No. 6.4%;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 202 MALPPCHTM 210

RESULT 15  
 US-09-083-541-3  
 Sequence 3, Application US/09083541  
 Patent No. 6323390

GENERAL INFORMATION:  
 APPLICANT: WU, Xue-Ru  
 ADDRESS: SUN, Tung-Tien  
 TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR HUMAN  
 TITLE OF INVENTION: BLADDER CANCER  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 STREET: 4119 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/083,541  
 PRIORITY CLAIM:  
 PRIOR APPLICATION DATA:  
 CLASSIFICATION:  
 PRIORITY CLAIM:  
 APPLICATION NUMBER: US 08/969,315  
 FILING DATE: 13-NOV-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: WU-42  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 3:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-083-541-3

RESULT 16
US-08-907-800A-2
Sequence 2, Application US/08907800A
Patent No. 6001646
GENERAL INFORMATION:
APPLICANT: SUN, Tung-Tien
TITLE OF INVENTION: METHOD AND VECTOR FOR EXPRESSION AND
ISOLATION OF BIOLOGICALLY ACTIVE MOLECULES IN URINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,800A
FILING DATE: 08-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,961
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SUN=9A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-907-800A-2

Query Match    78.6%; Score 44; DB 2; Length 44;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LMALPCH 8
Db      19 LIALPCH 26

RESULT 17
US-08-969-3117-2
Sequence 2, Application US/08969317

```

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; Patent No. 6227968
; GENERAL INFORMATION:
; APPLICANT: Tung-Tien Sun, Xue-Ru Wu
; TITLE OF INVENTION: Methods of Detecting and Classifying
; TITLE OF INVENTION: Bladder Cancer
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

; COMPUTER READABLE FORM:
; COMPUTER TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,317
; FILING DATE: herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: NYU-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; US-08-969-317-2

; RESULT 1.8
; Query Match 78.6%; Score 44; DB 2; Length 184;
; Best Local Similarity 87.5%; Pred. No. 7.8;
; Matches 7; Conservative 1; Mismatches 0; Indels
; 1 LMALPPCH 8
; :||| | |
; Db 45 LVALPPCH 52

; US-09-540-236-2576
; Sequence 2576, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATED TO THE THERAPEUTICS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2004-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO: 2576
; LENGTH: 282
; TYPE: PRT
; ORGANISM: M. catarrhialis
; US-09-540-236-2576

; RESULT 1.8
; Query Match 78.6%; Score 44; DB 2; Length 282;
; Best Local Similarity 77.8%; Pred. No. 12;
; Matches 7; Conservative 1; Mismatches 1; Indels
; 2 MALPCHAL 10
; :||| | |
; Db 159 VALPSCHTL 167

; Qy

```



Query Match 71.4%; Score 40; DB 2; Length 118;  
 Best Local Similarity 85.7%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 3 ALPPCHA 9  
 Db 9 ALPPCHS 15

RESULT 24  
 US-09-489-039A-10055  
 Sequence 10055, Application US/09489039A

GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 TITLE OF INVENTION: PNEUMONIAF FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2709-2004001  
 CURRENT APPLICATION NUMBER: US/09/489,039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 10055  
 LENGTH: 266  
 TYPE: PRT  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-10055

Query Match 71.4%; Score 40; DB 2; Length 266;  
 Best Local Similarity 87.5%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0;  
 Gaps 0;

Qy 2 MALPPCHA 9  
 Db 143 MALAPCHA 150

RESULT 25  
 US-09-614-912-8  
 Sequence 8, Application US/09614912

GENERAL INFORMATION:  
 APPLICANT: Allen, Steve  
 APPLICANT: Rafalski, Antoni  
 APPLICANT: Orozco, Buddy  
 APPLICANT: Miao, Gou-Hau  
 APPLICANT: Pamodu, Onchayao O.  
 APPLICANT: Lee, Jian Ming  
 APPLICANT: Sakai, Hajime  
 APPLICANT: Weng, Zude  
 APPLICANT: Caim, Perry G  
 APPLICANT: Anderson, Shawn  
 TITLE OF INVENTION: Plant Metabolism Genes  
 FILE REFERENCE: BB1378 US NA  
 CURRENT APPLICATION NUMBER: US/09/614,912  
 CURRENT FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: 60/143,401  
 PRIOR FILING DATE: 1999-07-12  
 PRIOR APPLICATION NUMBER: 60/143,412  
 PRIOR FILING DATE: 1999-07-12  
 PRIOR APPLICATION NUMBER: 60/146,650  
 PRIOR FILING DATE: 1999-07-30  
 PRIOR APPLICATION NUMBER: 60/170,906  
 PRIOR FILING DATE: 1999-12-15  
 PRIOR APPLICATION NUMBER: 60/172,959  
 PRIOR FILING DATE: 1999-12-21  
 PRIOR APPLICATION NUMBER: 60/172,946  
 PRIOR FILING DATE: 1999-12-21  
 NUMBER OF SEQ ID NOS: 204  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO 8  
 LENGTH: 351;

Query Match 69.6%; Score 39; DB 2; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 5 PPCHAL 10  
 Db 209 PPCHAI 214

RESULT 26  
 US-08-477-451-12  
 Sequence 12, Application US/08477451  
 Patent No. 5928855  
 GENERAL INFORMATION:  
 APPLICANT: Covacci, Antonello  
 TITLE OF INVENTION: Helicobacter Pylori CagI Region  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Chiron Corporation  
 STREET: 4560 Horton Street  
 CITY: Emeryville  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94608-2916  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,451  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McCling, Barbara G.  
 REGISTRATION NUMBER: 33,113  
 REFERENCE/DOCKET NUMBER: 0335.002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 510-601-2708  
 TELEFAX: 510-655-3542  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1720 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-477-451-12

Query Match 66.1%; Score 37; DB 1; Length 1720;  
 Best Local Similarity 83.3%; Pred. No. 8.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 5 PPCHAL 10  
 Db 1074 PPCHAI 1079

RESULT 27  
 US-09-959-392-20  
 Sequence 20, Application US/09959392  
 Patent No. 6806075  
 GENERAL INFORMATION:  
 APPLICANT: Morsier, Michael John  
 APPLICANT: Wu, Qingyu  
 APPLICANT: Yan, Wei  
 TITLE OF INVENTION: CORIN, A SERINE PROTEASE  
 FILE REFERENCE: BERLX 74A  
 CURRENT APPLICATION NUMBER: US/09/959,392

CURRENT FILING DATE: 2001-10-25  
 PRIORITY APPLICATION NUMBER: PCF/EP99/038895  
 PRIOR FILING DATE: 1999-06-04  
 PRIORITY APPLICATION NUMBER: 09/092,029  
 PRIORITY APPLICATION NUMBER: 09/314,967  
 PRIORITY FILING DATE: 1999-05-20  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 20  
 LENGTH: 102  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-959-332-20

Query Match Score 36; DB 2; Length 102;  
 Best Local Similarity 75.0%; Pred. No. 84;  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;  
 Qy 3 ALPPCHAL 10  
 Db 68 ALPPCRSL 75

RESULT 28  
 US-09-087-031B-16  
 Sequence 16, Application US/09087031E  
 Patent No. 6479255  
 GENERAL INFORMATION:  
 APPLICANT: Rubin, Jeffrey S.  
 APPLICANT: Finch, Paul  
 APPLICANT: Aaronson, Stuart  
 APPLICANT: He, Xi

TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM  
 FILE REFERENCE: 11613.13US11  
 CURRENT APPLICATION NUMBER: US/09/087,031E  
 CURRENT FILING DATE: 1998-05-29  
 PRIOR APPLICATION NUMBER: 09/087,031  
 PRIOR FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 16  
 LENGTH: 111  
 TYPE: PRT  
 ORGANISM: Rat

US-09-087-031B-16  
 Query Match Score 36; DB 2; Length 111;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 3 ALPPCHAL 10  
 Db 68 ALPPCRSL 75

RESULT 29  
 US-10-014-055-5  
 Sequence 5, Application US/10014055  
 Patent No. 6884871  
 GENERAL INFORMATION:  
 APPLICANT: Luyten, Frank P.  
 Hoang, Bang  
 Moos, Jr., Malcolm  
 Wang, Shouwen  
 TITLE OF INVENTION: ISOLATION AND USE OF TISSUE GROWTH INDUCING FRZB PROTEIN  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/014,055  
 FILING DATE: 07-Dec-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/729,452  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bartfeld, Neil S.  
 REGISTRATION NUMBER: 39,901  
 REFERENCE/DOCKET NUMBER: NIH133.001A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-235-8550  
 TELEFAX: 619-235-0176  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 111 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-10-014-055-5  
 Query Match Score 36; DB 2; Length 111;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 ALPPCHAL 10  
 Db 68 ALPPCRSL 75  
 RESULT 30  
 US-10-028-051A-5  
 Sequence 5, Application US/10028051A  
 Patent No. 6924367  
 GENERAL INFORMATION:  
 APPLICANT: Luyten, Frank P.  
 APPLICANT: Moos, Malcolm J.R.  
 APPLICANT: Hoang, Bang  
 APPLICANT: Wang, Shouwen  
 TITLE OF INVENTION: ISOLATION AND USE OF TISSUE  
 TITLES OF INVENTION: GROWTH-INDUCING FRZB PROTEIN  
 FILE REFERENCE: NIH133.1CPC1  
 CURRENT APPLICATION NUMBER: US/10/028,051A  
 CURRENT FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: US 08/822333  
 PRIOR FILING DATE: 1997-03-20  
 PRIOR APPLICATION NUMBER: US 08/729,452  
 PRIOR FILING DATE: 1996-10-11  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 5  
 LENGTH: 111  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-028-051A-5  
 Query Match Score 36; DB 2; Length 111;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHAL 10  
Db 68 ALPPCRSL 75

RESULT 31  
US-09-902-540-15035  
; Sequence 15035, Application US/09902540  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10 (15849) B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15035  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15035

Query Match 64.3%; Score 36; DB 2; Length 246;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;  
Matches 7; Conservative 1; Indels 0;

Qy 2 MALPPCHA 9  
Db 65 MALPPGHA 72

RESULT 32  
US-08-256-747C-76  
; Sequence 76, Application US/08256747C  
; Patent No. 6037448  
; GENERAL INFORMATION:  
; ADDRESSSE: Sim & McBurney  
; STREET: 6th Floor 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,747C  
; FILING DATE: 06-OCT-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I.  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-370  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-256-747C-76

Query Match 64.3%; Score 36; DB 2; Length 257;  
Best Local Similarity 85.7%; Pred. No. 2e+02; Mismatches 0; Gaps 0;  
Matches 6; Conservative 1; Indels 0;

Qy 3 ALPPCHA 9  
Db 121 APPCHA 127

RESULT 33  
US-09-902-540-15709  
; Sequence 15709, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10 (15849) B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15709  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15709

Query Match 64.3%; Score 36; DB 2; Length 463;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 0; Gaps 0;  
Matches 5; Conservative 1;

Qy 5 PPCHAL 10  
Db 80 PPCHSL 85

RESULT 34  
US-08-313-200-1  
; Sequence 1, Application US/08313200  
; Patent No. 5981653  
; GENERAL INFORMATION:  
; APPLICANT: Baker, James R.  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/313,200  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Konski, Antoinette F.  
; REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 20344-20658.20  
 TELECOMMUNICATION ID: 456..633  
 TELEPHONE: (415) 813-5600  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 933 amino acids  
 TYPE: amino-acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 DEVELOPMENTAL STAGE: Mature  
 TISSUE TYPE: Thyroid gland (From people with Grave's disease)  
 IMMEDIATE SOURCE:  
 CLONE: pHTPO-2.8  
 FEATURES:  
 NAME/KEY: Peptide  
 LOCATION: join(1..3, 456..631)  
 OTHER INFORMATION: /note= "TPO region within fusion  
 OTHER INFORMATION: plasmid: TPO(delta4-455)"  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..120  
 OTHER INFORMATION: /note= "C-terminal truncation:  
 OTHER INFORMATION: TPO(1..120)"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1..400  
 OTHER INFORMATION: /note= "TPO epitopic region within  
 OTHER INFORMATION: fusion protein: MBP-TPO (AA 1-400)"  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..455  
 OTHER INFORMATION: /note= "C-terminal truncation-  
 OTHER INFORMATION: TPO(1..455) or N-terminal half of TPO"  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..631  
 OTHER INFORMATION: /note= "C-terminal truncation:  
 OTHER INFORMATION: TPO(1..631)"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 265..281  
 OTHER INFORMATION: /note= "TPO epitopic or binding  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 376..631  
 OTHER INFORMATION: /note= "TPO epitopic region within  
 OTHER INFORMATION: fusion protein: MBP-TPO (AA 376-631)"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: join(455..532, 590..933)  
 OTHER INFORMATION: /note= "alternatively spliced  
 OTHER INFORMATION: C-terminus of TPO"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 455..933  
 OTHER INFORMATION: /note= "TPO C-terminus containing  
 OTHER INFORMATION: binding region"  
 FEATURE:

NAME/KEY: Region  
 LOCATION: 456..633 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 FEATURES:  
 NAME/KEY: Region  
 LOCATION: 456..933  
 OTHER INFORMATION: /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 456..933 /note= "TPO region within maltose  
 OTHER INFORMATION: binding fusion protein"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 457..517 /note= "non-reactive fragment"  
 OTHER INFORMATION: /note= "non-reactive fragment"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 457..633 /note= "TPO region within fusion  
 OTHER INFORMATION: plasmid pMalTPO"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 457..933 /note= "TPO binding region within  
 OTHER INFORMATION: plasmid pMalTPO"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 465..933 /note= "TPO binding region of  
 OTHER INFORMATION: maltose binding region fusion construct"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 511..633 /note= "recombinant TPO"  
 OTHER INFORMATION: /note= "recombinant TPO"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 511..633 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 511..630 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 573..633 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 590..611 /note= "TPO region within maltose  
 OTHER INFORMATION: binding fusion protein"  
 FEATURE:  
 NAME/KEY: Binding-site  
 LOCATION: 590..675 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 OTHER INFORMATION: region"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 591..613 /note= "TPO binding or epitopic  
 OTHER INFORMATION: region"  
 OTHER INFORMATION: region"

```

RESULT 36
US-09-949-016-5953 ; Sequence 593, Application US/09949016
; Patent No. 6812319 ; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5953
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5953

Query Match
Best Local Similarity 85.7%; Score 36; DB 2; Length 933;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 37
US-09-949-016-7322 ; Sequence 7322, Application US/09949016
; Patent No. 6812319 ; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7322
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7322

Query Match
Best Local Similarity 85.7%; Score 36; DB 2; Length 933;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 38
PCT-US93-03837-1 ; Sequence 1, Application PC/TUS9303837
; GENERAL INFORMATION:
; APPLICANT: Baker, Jr., James R.
; APPLICANT: Koenig, Ronald J.
; APPLICANT: University of Michigan
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPE REGIONS
; FILE REFERENCE: 20442065801
; CURRENT APPLICATION NUMBER: US/09/251,039
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/513,200
; EARLIER FILING DATE: 1994-11-08
; EARLIER APPLICATION NUMBER: 07/885,656
; EARLIER FILING DATE: 1992-05-19
; EARLIER APPLICATION NUMBER: PCT/US93/03837
; EARLIER FILING DATE: 1993-04-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-251-039-2

Query Match
Best Local Similarity 85.7%; Score 36; DB 2; Length 933;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 3 ALPPCHA 9
Db 804 AHPPCHA 810

Query Match
Best Local Similarity 85.7%; Score 36; DB 2; Length 933;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 3 ALPPCHA 9
Db 804 AHPPCHA 810

```

APPLICANT: Koenig, Ronald J. Thyroid Peroxidase Epitopic Regions  
 TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Harness, Dickey & Pierce  
 STREET: P.O. Box 828  
 CITY: Bloomfield Hills  
 STATE: MI  
 COUNTRY: USA  
 ZIP: 48303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOC/MS-DOS  
 SOFTWARE: PatentIn Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/03837  
 FILING DATE: 19930422  
 CLASSIFICATION INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lewak, Anna M.  
 REGISTRATION NUMBER: 33006  
 REFERENCE/DOCKET NUMBER: 2115-00658PPA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (313) 641-1600  
 TELEFAX: (313) 641-0270  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 933 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 DEVELOPMENTAL STAGE: Mature  
 TISSUE TYPE: Thyroid Gland (from people with Grave's  
 TISSUE TYPE: disease)  
 IMMEDIATE SOURCE:  
 CLONE: PHTP0-2.8  
 PUBLICATION INFORMATION:  
 AUTHORS: Kimura, S.  
 AUTHORS: Kotani, T.  
 AUTHORS: McBride, O. W.  
 AUTHORS: Umeki, K.  
 AUTHORS: Nakayama, T.  
 AUTHORS: Ohatai, S.  
 AUTHORS: Hirai, K.  
 TITLE: Human thyroid peroxidase: Complete cDNA and  
 TITLE: identification of two alternatively spliced mRNAs  
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
 VOLUME: 84  
 PAGE: 5555-5559  
 DATE: 1987  
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048  
 PCT-US93/03837-1

Query Match Score 36; DB 4; Length 933;  
 Best Local Similarity 85.7%; Pred. No. 6.7e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9  
 Db 804 AHPCHA 810

RESULT 39  
 US-10-734-049b-188.ra1

Query Match Score 36; DB 1; Length 992;  
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9  
 Db 804 AHPCHA 810

GENERAL INFORMATION:

```

Db      419 APPCCHA 425
RESULT 41
US-08-482-847-1
; Sequence 1, Application US/08482847
; GENERAL INFORMATION:
;   APPLICANT: VAN ALSTYNE, Diane
;   APPLICANT: SHARMA, Lawrence Rajendra
;   TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPE SITES FOR
;   TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
;   TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US 08/482,847
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/127,499
;       FILING DATE: 28-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME: BENT, Stephen A.
;       REGISTRATION NUMBER: 29,768
;       REFERENCE/DOCKET NUMBER: 5916/104/INBI
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202)672-5300
;       TELEFAX: (202)672-5399
;     INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 992 amino acids
;         TYPE: amino acid
;         STRANDEDNESS:
;         TOPOLOGY: unknown
;     US-08-482-847-1

Query Match Score 36%; Pred. No. 7.1e+02; Length 992;
Best Local Similarity 85.7%; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Db      3 ALPPCHA 8
Db      11 APPCCHA 16
Db      11 APPCCHA 16

RESULT 43
US-09-534-638-5
; Sequence 5, Application US/09534638
; GENERAL INFORMATION:
;   APPLICANT: Pannia, Pertti A.J.
;   APPLICANT: Brandt, Annika
;   APPLICANT: Westerlund, Johanna
;   TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
;   TITLE OF INVENTION: for therapy and diagnosis
;   FILE REFERENCE: 2530-104
;   CURRENT APPLICATION NUMBER: US/09/514,638
;   CURRENT TILING DATE: 2000-03-27
;   EARLIER APPLICATION NUMBER: 09/365755
;   EARLIER FILING DATE: 1999-08-03
;   NUMBER OF SEQ ID NOS: 22
;   SEQ ID NO 5
;   LENGTH: 129
;   TYPE: PRT
;   SOFTWARE: PatentIn Ver. 2.1
;     ORGANISM: Mouse
;     US-09-534-638-5

Query Match Score 35%; Pred. No. 1.5e+02;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Db      4 LPPCHA 8
Db      91 LPPCHA 95

RESULT 44
US-09-270-767-57195
; Sequence 57195, Application US/09270767
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SEQ ID NO 57195
;   LENGTH: 212
;   TYPE: PRT
;   SOFTWARE: PatentIn Ver. 2.0
;     ORGANISM: Drosophila melanogaster
;     US-09-270-767-57195

Query Match Score 35%; Pred. No. 2.4e+02;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      3 ALPPCHA 9
Db      419 APPCCHA 425

RESULT 42
US-10-360-101-162
; Sequence 162, Application US/10360101
; GENERAL INFORMATION:
;   APPLICANT: Moll, Gert N.
;   APPLICANT: Leenhoux, Cornelis J.
;   TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
;   FILE REFERENCE: 21.8-3-5673
;   CURRENT APPLICATION NUMBER: US/10/360,101
;   CURRENT FILING DATE: 2003-02-07
;   PRIOR APPLICATION NUMBER: EP 02077060.8
;   PRIOR FILING DATE: 2002-05-24
;   NUMBER OF SEQ ID NOS: 309
;   SOFTWARE: PatentIn version 3.1
;     ORGANISM: Xaa means any amino acid
;     US-09-270-767-57195

```

Qy 4 LPPCH 8  
 Db 186 LPPCH 190

RESULT 45  
 US-09-949-016-7312  
 ; Sequence 7312, Application US/09949016  
 ; GENERAL INFORMATION  
 ; APPLICANT: VENTIER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/949.016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIORITY APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIORITY APPLICATION NUMBER: 60/231,498  
 ; PRIORITY FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 7312  
 ; LENGTH: 214  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-7312

Query Match 62.5%; Score 35; DB 2; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LPPCH 8  
 Db 10 LPPCH 14

RESULT 46  
 US-09-270-767-39225  
 ; Sequence 39225, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270.767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SEQ ID NO: 39225  
 ; LENGTH: 268  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-39225

Query Match 62.5%; Score 35; DB 2; Length 268;  
 Best Local Similarity 50.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LMLAPPCHAL 10  
 Db 50 IFALPSCHCI 59

RESULT 47  
 US-09-270-767-54442  
 ; Sequence 54442, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION

```

Query Match      62.5%;  Score 35;  DB 2; Length 276;
Best Local Similarity   83.4%;  Pred. No. 3.1e+02;  Indels 0;  Gaps 0;
Matches      5;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      5  PPCHAL 10
Db     103  PPCHGL 108

```

---

```

RESULT 50
US-09-902-540-16237
; Sequence 16237, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16237
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
us-09-902-540-16237

```

```

Query Match      62.5%;  Score 35;  DB 2; Length 281;
Best Local Similarity   85.7%;  Pred. No. 3.1e+02;  Indels 0;  Gaps 0;
Matches      6;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      3  ALPPCHA 9
Db     201  ALPACHA 207

```

Search completed: February 17, 2006, 02:45:24  
Job time : 60 secs

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## OM protein - protein search, using SW model

Run on: February 17, 2006, 02:40:31 ; Search time 38 Seconds

(without alignments)  
25.320 Million cell updates/sec

Title: US-10-734-049B-188

Perfect score: 56  
Sequence: 1 LMAPPCHAL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80:  
1: Pir1:  
2: Pir2:  
3: Pir3:  
4: Pir4:  
5: Pir5:  
6: Pir6:  
7: Pir7:  
8: Pir8:  
9: Pir9:  
10: Pir10:  
11: Pir11:  
12: Pir12:  
13: Pir13:  
14: Pir14:  
15: Pir15:  
16: Pir16:  
17: Pir17:  
18: Pir18:  
19: Pir19:  
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96: Pir96:  
97: Pir97:  
98: Pir98:  
99: Pir99:  
100: Pir100:  
101: Pir101:  
102: Pir102:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	307	1 YXMST	thymidylate synthase
2	56	100.0	307	2 S53715	thymidylate synthase
3	56	100.0	313	1 YXHUT	thymidylate synthase
4	52	92.9	264	2 G81050	thymidylate synthase
5	52	92.9	264	2 A81825	thymidylate synthase
6	52	92.9	264	2 D83802	thymidylate synthase
7	49	87.5	314	2 AB1309	thymidylate synthase
8	49	87.5	314	2 AB1681	thymidylate synthase
9	48	85.7	263	2 C70881	probable thymidylate synthase
10	48	85.7	264	1 S35239	thymidylate synthase
11	48	85.7	264	2 A12227	thymidylate synthase
12	48	85.7	264	2 AB3328	thymidylate synthase
13	48	85.7	266	2 A87099	thymidylate synthase
14	48	85.7	279	2 G97605	hypothetical prote
15	48	85.7	279	2 C87512	thymidylate synthase
16	48	85.7	290	1 SYBEAT	thymidylate synthase
17	48	85.7	290	2 T42284	thymidylate synthase
18	48	85.7	301	1 SYBEI3	thymidylate synthase
19	48	85.7	316	1 SYLBET	thymidylate synthase
20	48	85.7	518	2 T05277	dihydrofolate redu
21	48	85.7	519	2 E84539	dihydrofolate redu
22	48	85.7	528	2 S35272	dihydrofolate redu
23	48	85.7	530	2 S55683	dihydrofolate redu
24	48	85.7	577	2 T14315	dihydrofolate redu
25	47	83.9	289	2 S55667	thymidylate synthase
26	47	83.9	387	2 E75520	thymidylate synthase
27	47	83.9	520	1 RDINTS	dihydrofolate redu
28	47	83.9	520	1 RDINTZ	dihydrofolate redu
29	47	83.9	583	1 RDZQTB	dihydrofolate redu

30	47	83.9	608	1 RDZQK1	dihydrofolate redu
31	47	83.9	610	2 A45005	dihydrofolate redu
32	47	83.9	623	2 JC5568	thymidylate synthase
33	46	82.1	318	1 YXSAT3	dihydrofolate redu
34	46	82.1	318	2 CB9920	thymidylate synthase
35	46	82.1	462	2 S65570	dihydrofolate redu
36	44	78.6	184	2 T09609	uroplakin II - hum
37	44	78.6	184	2 AJ5135	uroplakin II precu
38	44	78.6	184	2 JC7839	uroplakin II precu
39	44	78.6	185	2 A49713	thymidylate synthase
40	44	78.6	259	1 YABVT	dihydrofolate redu
41	44	78.6	286	1 SYBPT4	thymidylate synthase
42	44	78.6	294	1 SYBEHS	thymidylate synthase
43	44	78.6	297	1 YKONTP	thymidylate synthase
44	44	78.6	315	1 YCKTKA	thymidylate synthase
45	44	78.6	328	2 S73842	thymidylate synthase
46	44	78.6	521	2 T01684	dihydrofolate redu
47	44	78.6	625	2 T37719	thymidylate synthase
48	43	76.8	264	2 GB8569	thymidylate synthase
49	43	76.8	264	2 B84981	thymidylate synthase
50	43	76.8	286	2 B90579	thymidylate synthase
51	42	75.0	315	2 T52178	thymidylate synthase
52	41	73.2	287	2 A61225	thymidylate synthase
53	40	71.4	264	1 SYBSTD	hypothetical prote
54	40	71.4	264	1 SYBCT	hypothetical prote
55	40	71.4	264	2 AB0866	hypothetical prote
56	40	71.4	264	2 AB0096	hypothetical prote
57	40	71.4	264	2 C84081	DNA mismatch repair
58	40	71.4	264	2 F85934	ORF MSV238 probable
59	40	71.4	264	2 D91089	conserved hypothetical
60	39	69.6	336	2 AB1152	calf thymus ribonu
61	38	67.9	233	2 AB1152	structural polypro
62	38	67.9	233	2 AB1152	structural polypro
63	38	67.9	292	2 T2839	structural polypro
64	38	67.9	395	2 BB3326	structural polypro
65	37	66.1	220	2 AH3444	structural polypro
66	37	66.1	275	2 T04480	structural polypro
67	36	64.3	307	2 T27061	hypothetical prote
68	36	64.3	358	2 A39467	hypothetical prote
69	36	64.3	635	2 AC0046	hypothetical prote
70	36	64.3	641	2 A45054	hypothetical prote
71	36	64.3	647	2 JB0337	Frizzled-1 protein
72	36	64.3	933	1 -OPHUIT-	Frizzled-1 protein
73	36	64.3	992	1 GNWVR3	iodide peroxidase
74	36	64.3	1063	1 GNWV77	iodide peroxidase
75	36	64.3	1063	1 GNWV77	dynein heavy chain
76	35	62.5	170	2 TS0164	probable cleavage
77	35	62.5	196	2 A30327	corticoline pre
78	35	62.5	309	2 DB40776	homoserine kinase
79	35	62.5	358	2 BT1686	hypothetical prote
80	35	62.5	377	2 T34272	hypothetical prote
81	35	62.5	444	2 T22412	hypothetical prote
82	35	62.5	457	2 T21063	hypothetical prote
83	35	62.5	639	1 S45776	uracil transport p
84	35	62.5	926	1 OPPGTT	iodide peroxidase
85	35	62.5	1116	2 RSHHC	cobalamin biosynth
86	35	62.5	1116	2 D97695	cobN protein homol
87	35	62.5	1650	2 NADH2 dehydrogenas	dominant autoantig
88	35	62.5	349	2 T11128	o-succinylbenzoic
89	35	62.5	368	2 B87191	RNA polymerase I-
90	34	60.7	5376	2 T42215	zonadhesin - mouse
91	34	60.7	140	2 C69269	hypothetical prote
92	34	60.7	190	1 RSHHC	corticoline pre
93	34	60.7	295	2 S23956	beta-chimerin - ra
94	34	60.7	349	2 T11128	beta-chimerin - ra
95	34	60.7	4660	2 T42237	beta-chimerin - ce
96	34	60.7	434	2 S62445	beta2-chimerin, ce
97	34	60.7	443	2 B53764	beta2-chimerin, ce
98	34	60.7	518	1 S44183	thiamine-phosphate
99	34	60.7	574	2 T3339	Frizzled-7 protein
100	34	60.7	733	2 AG33761	peptidyl-dipeptida
101	34	60.7	976	2 S45738	pleiotropic drug r
102	34	60.7	1102	2 A84480	probable retroelement

103	34	60.7	1239	2	G71266	probable ATP-depen
104	33	60.7	1596	2	A35927	190K DNA-binding p
105	33	59.8	741	2	B69400	molybdopterin oxid
106	33	58.9	65	2	S35172	cytochrome P450 (c
107	33	58.9	109	2	G81244	phna protein NBB00
108	33	58.9	109	2	F82023	Phna protein homol
109	33	58.9	137	2	S28705	hypothetical prote
110	33	58.9	137	2	E72459	Frizzled-2 prote
111	33	58.9	183	2	C94935	4-coumarate-CoA li
112	33	58.9	198	2	B83266	-
113	33	58.9	256	2	H82525	probable transposo
114	33	58.9	294	2	G72706	anthranilate synth
120	33	58.9	499	2	T09656	hypothetical prote
121	33	58.9	311	2	D87164	hypothetical prote
122	33	58.9	618	2	T42664	NADH2 dehydrogenas
123	33	58.9	623	2	S55652	hypothetical prote
124	33	58.9	655	2	A40675	hypothetical prote
125	33	58.9	656	2	S55262	uracil-DNA glycosy
126	33	58.9	688	2	B65005	hypothetical prote
127	33	58.9	688	2	H91029	ory protein homol
128	33	58.9	749	2	A95953	probable LysR-tami
129	33	58.9	1129	2	T42732	N-acetyl-gamma-glu
130	33	58.9	1174	1	A43736	hypothetical prote
131	33	58.9	1224	2	T26377	acetyl-CoA-deacetyl
132	33	58.9	1670	2	T06754	hypothetical prote
133	32	57.1	72	2	S49021	beta 1,3-Glucanase
134	32	57.1	74	2	S13515	probable peptidase
135	32	57.1	89	2	S13517	bifunctional prote
136	32	57.1	96	2	T03290	transcription cont
137	32	57.1	141	2	AB3275	nuclear anchoring
138	32	57.1	143	1	Q9VLCP	A-kinase anchoring
139	32	57.1	154	1	Q0V006	creatine kinase (C
140	32	57.1	171	2	T28000	hypothetical prote
141	32	57.1	175	2	T5143	hypothetical prote
142	32	57.1	178	2	T28045	probable lipid tra
143	32	57.1	182	2	A53803	hypothetical prote
144	32	57.1	224	2	AD1114	probable olfactory
145	32	57.1	224	2	AE1475	probable olfactory
146	32	57.1	236	2	I59323	gene X protein - h
147	32	57.1	257	2	T51726	hypothetical prote
148	32	57.1	261	2	S63604	auxin-induced prot
149	32	57.1	262	2	T42986	probable lipid tra
150	32	57.1	264	2	F22714	dihydrofolate redu
151	32	57.1	273	2	I48187	thiamin biosynthes
152	32	57.1	273	2	JCA634	thiamin biosynthes
153	32	57.1	275	2	A82578	apolipoprotein B m
154	32	57.1	292	2	D85863	probable cobalt tr
155	32	57.1	292	2	B91019	homeobox protein G
156	32	57.1	327	2	JT0584	v-cyclin - atelina
157	32	57.1	337	2	A12360	hypothetical prote
158	32	57.1	341	2	S51766	hypothetical prote
159	32	57.1	343	2	T02071	glycerol uptake fa
160	32	57.1	343	2	D89605	probable regulator
161	32	57.1	352	1	H81165	probable transcript
162	32	57.1	352	1	A34933	deoxyribonuclease
163	32	57.1	356	2	D65096	hypothetical prote
164	32	57.1	356	2	H85968	dioxxygenase - eggp
165	32	57.1	356	2	A98124	glyceraldehyde-3-p
166	32	57.1	362	2	B83282	protein F18G5.3 [1
167	32	57.1	365	2	B39467	modification methyl
168	32	57.1	372	2	S77549	glycoprotein-fucos
169	32	57.1	400	2	A61297	hypothetical 40.1
170	32	57.1	413	1	S39554	hypothetical prote
171	32	57.1	413	1	A34888	transcription fact
172	32	57.1	419	2	F96704	hypothetical prote
173	32	57.1	435	2	G90700	probable uracil tr
174	32	57.1	435	2	B85551	probable transport
175	32	57.1	435	2	H64782	probable membrane
176	32	57.1	439	2	A84431	probable C2H2-type
177	32	57.1	468	2	B70899	probable FB prote
178	32	57.1	468	2	JX0065	anthranilate synth
179	32	57.1	494	2	T00400	hypothetical prote
180	32	57.1	505	2	T50606	hypothetical prote
181	32	57.1	538	2	JB0338	Frizzled-2 prote
182	32	57.1	565	2	F85214	4-coumarate-CoA li
183	32	57.1	566	2	B85013	probable transposo
184	32	57.1	566	2	T0538	hypothetical prote
185	32	57.1	586	2	A85057	hypothetical prote
186	32	57.1	592	2	T40040	GTpase-activator P
187	32	57.1	632	2	S64786	iodide peroxidase
188	32	57.1	655	2	T16538	hypothetical prote
189	32	57.1	662	2	S62707	NADH2 dehydrogenas
190	32	57.1	672	2	T25876	hypothetical prote
191	32	57.1	672	2	B85013	hypothetical prote
192	32	57.1	693	2	T10539	hypothetical prote
193	32	57.1	704	2	T30257	IGG FC binding pro
194	32	57.1	704	2	D84900	hypothetical prote
195	32	57.1	710	2	A81368	probable 2-acylgly
196	32	57.1	710	2	JC5368	dynactin 1 - mouse
197	32	57.1	710	2	T18939	hypothetical prote
198	32	57.1	710	2	S16129	adenomatus polypo
199	32	57.1	710	2	T13825	hypothetical prote
200	32	57.1	710	2	T09144	sensor protein lim
201	32	57.1	710	2	A08660	sensor protein -
202	32	57.1	710	2	B44008	lethal peptide I -
203	32	57.1	710	2	A44008	lethal peptide II
204	32	57.1	710	2	T37138	hypothetical prote
205	32	57.1	710	2	C41397	hypothetical prote
206	32	56.2	710	2	JC1126	major allergen cha
207	31	55.4	710	2	KRSHH4	keratin high-sulfu
208	31	55.4	710	2	I47086	BRILB4 high-sulfur
209	31	55.4	710	2	E71153	hypothetical prote
210	31	55.4	710	2	D42409	biphenyl dioxygena
211	31	55.4	710	2	E41858	biphenyl dioxygena
212	31	55.4	710	2	T36789	hypothetical prote
213	31	55.4	710	2	T49382	hypothetical prote
214	31	55.4	710	2	S50867	4E-BP2 protein - h
215	31	55.4	710	2	T49467	hypothetical prote
216	31	55.4	710	2	B82865	conserved hypotet
217	31	55.4	710	2	B93363	protein limpop
218	31	55.4	710	2	AF2547	hypothetical prote
219	31	55.4	710	2	B85666	cysteine proteinas
220	31	55.4	710	2	D91147	corticoline protein
221	31	55.4	710	2	A45362	hypothetical prote
222	31	55.4	710	2	B22990	ZC262.4 protein -
223	31	55.4	710	2	S22990	zein, 27K - maize
224	31	55.4	710	2	T34664	methylated-DNA-Ipr
225	31	55.4	710	2	AP1010	conserved hypothet
226	31	55.4	710	2	JC4269	hypothetical prote
227	31	55.4	710	2	B85992	hypothetical prote
228	31	55.4	710	2	E65120	hypothetical prote
229	31	55.4	710	2	B82591	hypothetical prote
230	31	55.4	710	2	A53853	hypothetical prote
231	31	55.4	710	2	T33855	hypothetical prote
232	31	55.4	710	2	S74620	hypothetical prote
233	31	55.4	710	2	B85950	hypothetical lipop
234	31	55.4	710	2	E91105	apolipoprotein B m
235	31	55.4	710	2	B85951	apolipoprotein B m
236	31	55.4	710	2	B85952	hypothetical prote
237	31	55.4	710	2	B85953	hypothetical prote
238	31	55.4	710	2	B85954	hypothetical prote
239	31	55.4	710	2	B85955	hypothetical prote
240	31	55.4	710	2	T37811	hypothetical prote
241	31	55.4	710	2	A53853	hypothetical prote
242	31	55.4	710	2	S74620	hypothetical prote
243	31	55.4	710	2	B85950	hypothetical prote
244	31	55.4	710	2	E91105	hypothetical prote
245	31	55.4	710	2	A60533	tumor-associated a
246	31	55.4	710	2	T31305	4-hydroxy-2-oxoval
247	31	55.4	710	2	S44796	F09G8.6 protein -
248	31	55.4	710	2	GB5045	probable hydrolase

249	AP0123	291	probable antigenic protein	3068	1
250	T27090	298	hypothetical prote	31	A44062
251	T25610	299	alpha-conotoxin -	30.5	F32252
252	G71109	303	margatoxin [valida	54.5	53.6
253	D82786	311	hypothetical prote	39	A55877
254	T26673	315	thiamin biosynthes	1	A48523
255	T08807	316	hypothetical prote	45	T22203
256	T46544	321	mitochondrial prote	30	A48350
257	T04920	326	cyclase [imported]	30	AF2350
258	E93337	326	hypothetical prote	30	hypothetical prote
259	AE3945	338	thiamin biosynthes	30	hypothetical prote
260	S04280	338	hypothetical prote	30	hypothetical prote
261	S25267	345	cytSteine proteinas	30	probable olfactory
262	WMBB38	354	infected cell prot	30	hypothetical prote
263	H87575	354	polygalacturonase	30	hypothetical prote
264	S54213	362	fructose-bisphosph	30	hypothetical prote
270	T02057	362	probable zinc-bind	30	hypothetical prote
271	A70547	362	zinc-binding dehyd	30	hypothetical prote
272	WOUH	367	psbA intron 1 prot	30	hypothetical prote
273	T11849	370	gibberellin 20-oxi	30	probable olfactory
274	D86203	374	hypothetical prote	30	hypothetical prote
269	S54213	383	cellular biosynth	30	hypothetical prote
275	C82987	389	probable MFS trans	30	hypothetical prote
276	A27658	395	probable manE - My	30	hypothetical prote
277	T23461	395	alpha-2-HS-glycop	30	heparin-binding EG
278	H72654	395	gibberellin 20-oxi	30	hypothetical prote
279	A26371	403	steroid-bindin	30	hypothetical prote
280	D86203	412	hypothetical prote	30	hypothetical prote
281	T46333	414	polygalacturonase	30	hypothetical prote
282	S63513	414	probable isoctrat	30	hypothetical prote
283	D75469	435	hypothetical prote	30	halorhodopsin [val
277	T02057	441	hypothetical prote	30	ribosomal tRNA (guanine-N1) -
278	H70947	448	hypothetical prote	30	methylated-dNA [pr
279	A17501	456	sex steroid-bindin	30	probable tRNA (qua
280	T47633	464	probable hexosid	30	ribofuranose binding
281	S63513	476	hypothetical prote	30	hypothetical prote
282	D75469	477	L2 protein - human	30	hypothetical prote
283	E70508	487	probable regulator	30	hypothetical prote
284	S236390	489	hypothetical prote	30	halorhodopsin [val
285	T01235	492	mitochondrial prote	30	probable tRNA (guanine-N1) -
286	H86148	499	hypothetical prote	30	probable tRNA (guanine-N1) -
287	S27381	518	probable serine/th	30	probable tRNA (guanine-N1) -
288	T06134	524	hypothetical prote	30	probable tRNA (guanine-N1) -
289	T32812	530	hypothetical prote	30	probable tRNA (guanine-N1) -
290	T22021	531	hypothetical prote	30	probable tRNA (guanine-N1) -
291	A67118	556	squalene-hopene cy	30	probable tRNA (guanine-N1) -
292	A80046	556	probable N-acetyl	30	probable tRNA (guanine-N1) -
293	JC1282	593	insulin-like growth	30	probable tRNA (guanine-N1) -
294	S71630	603	metalloproteinase	30	probable tRNA (guanine-N1) -
295	AG0123	605	probable antigenic	30	probable tRNA (guanine-N1) -
296	H96766	623	unknown protein F2	30	probable tRNA (guanine-N1) -
297	A80123	626	probable antigenic	30	probable tRNA (guanine-N1) -
298	C87048	629	probable ABC trans	30	probable tRNA (guanine-N1) -
299	E72080	653	penicillin-binding	30	probable tRNA (guanine-N1) -
300	A86543	653	transglycolase/tra	30	probable tRNA (guanine-N1) -
301	T10567	666	probable serine/th	30	probable tRNA (guanine-N1) -
302	A49227	695	hypothetical prote	30	probable tRNA (guanine-N1) -
303	A27041	753	tyrosine kinase - re	30	probable tRNA (guanine-N1) -
304	F06387	760	probable Pro kinas	30	probable tRNA (guanine-N1) -
305	A82086	781	hypothetical prote	30	probable tRNA (guanine-N1) -
306	H96494	815	protein F7R2.2 [i	30	probable tRNA (guanine-N1) -
307	A39030	882	androgen-binding p	30	probable tRNA (guanine-N1) -
308	T42045	901	sialidase - Actino	30	probable tRNA (guanine-N1) -
309	H95973	901	fibulin-2 precursor	30	probable tRNA (guanine-N1) -
310	VGBBPS	913	glycoprotein GII P	30	probable tRNA (guanine-N1) -
311	JC3387	913	exo-alpha-sialidases	30	probable tRNA (guanine-N1) -
312	JN0550	914	iode peroxidase	30	probable tRNA (guanine-N1) -
313	A12126	1049	beta transducin-like	30	probable tRNA (guanine-N1) -
314	AE55194	1184	fibulin-2 precurs	30	probable tRNA (guanine-N1) -
315	B88557	1247	epidermal growth f	30	probable tRNA (guanine-N1) -
316	JC3387	1339	kinase-related tra	30	probable tRNA (guanine-N1) -
317	A16223	1342	NAP kinase kinase	30	probable tRNA (guanine-N1) -
318	T10757	1493	guanine nucleotide	30	probable tRNA (guanine-N1) -
319	A12126	1596	triptate dehydr	30	probable tRNA (guanine-N1) -
320	S05306	2318	gene frizzled pro-	30	probable tRNA (guanine-N1) -
321	T29140	2326	lisocitrate dehydr	30	probable tRNA (guanine-N1) -

395	53.6	586	2	AI2065	hypothetical prote	127	2	T31900
396	53.6	589	2	T01709	conserved hypothetical prote	129	2	H90161
397	53.6	592	2	S25705	Ig mu Chain - shee	129	2	51.8
398	53.6	593	2	AF1011	isocitrate dehydro	130	2	51.8
399	53.6	605	2	A48115	transcription fact	130	2	T06394
400	53.6	605	2	T01067	probable secretion	135	2	D82539
401	53.6	605	2	G70409	fact	146	2	H71557
402	53.6	608	2	S05341	high affinity sulf	150	2	JA0086
403	53.6	616	2	T19873	probable reverse t	154	2	T06396
404	53.6	627	2	T02846	hypothetical prote	157	2	S49622
405	53.6	630	1	S33539	dynamin light Chain	157	2	RC1725
406	53.6	652	2	F85017	catechol oxidase (	160	2	S66152
407	53.6	665	2	P84523	probable CHP-rich	161	2	S49488
411	53.6	712	2	T23738	membrane	161	2	S19370
412	53.6	711	2	T09082	hypothetical prote	164	2	C87526
413	53.6	752	2	JC4898	peptidoglycan-asso	172	2	C86588
414	53.6	754	2	A40351	peptidoglycan-asso	177	2	T26583
415	53.6	757	2	S17982	ubiquinol-cytocho	192	2	H72036
416	53.6	760	2	A10803	tein	192	2	A44033
417	53.6	767	2	E85079	hypothetical prote	198	2	E89871
418	53.6	780	2	T44218	conserved hypothetical prote	200	1	Q3ECPR
419	53.6	780	2	T44033	excinuclease ABC	206	1	XUBYMC
420	53.6	783	1	A38637	C	206	1	H91128
421	53.6	783	2	T30644	telomere-associate	209	1	G85973
422	53.6	797	2	T09081	Down-syndrome crit	210	2	H72585
423	53.6	801	2	AB1960	telomere-associate	212	2	H72036
424	53.6	823	2	F64526	hypothetical prote	212	2	A44033
425	53.6	850	2	TS1541	excinuclease ABC	212	2	E89871
426	53.6	867	2	T14777	hypothetical prote	212	2	FLT3/FLK2 ligand (
427	53.6	922	2	JCT083	origin binding pro	212	2	SL3413
428	53.6	964	2	T41547	Ras interactor RIN	212	2	B70790
429	53.6	966	1	P1BVBB	hypothetical prote	212	2	USP2 protein - mou
430	53.6	1040	2	T39936	protein disulfide	212	2	A44033
431	53.6	1056	2	T00060	hypothetical prote	212	2	arginine ABC trans
432	53.6	1134	2	A41350	protein disulfide	212	2	ubiquinol-cytocho
433	53.6	927	2	T45615	excinuclease ABC	212	2	FLT3/FLK2 ligand (
434	53.6	964	2	T02856	hypothetical prote	212	2	SL3413
435	53.6	1299	2	T18398	adenin/lysine D	212	2	B70790
436	53.6	1308	2	T18408	hypothetical prote	212	2	A44033
437	53.6	1342	2	T18405	protein kinase (BC	212	2	E89871
438	53.6	1351	2	T18409	excinuclease ABC	212	2	SL3413
439	53.6	1191	2	AP2501	hypothetical prote	212	2	B70790
440	53.6	1195	2	S76592	5-methyltetrahydro	212	2	A44033
441	53.6	1571	2	T18395	latrophilin-3, sp1	212	2	SL3413
442	53.6	1580	2	T18407	latrophilin-3, sp1	212	2	B70790
443	53.6	2176	2	T39188	latrophilin-3, sp1	212	2	A44033
444	53.6	2195	2	S61103	latrophilin-3, sp1	212	2	SL3413
445	53.6	2274	2	T30258	probable membrane	212	2	B70790
446	53.6	2347	2	T02856	latrophilin-3, sp1	212	2	A44033
447	53.6	4957	2	T03455	latrophilin-3, sp1	212	2	SL3413
448	53.6	5262	2	T03454	latrophilin-3, sp1	212	2	B70790
449	52.7	275	2	A82257	probable membrane	212	2	A44033
450	52.7	394	2	T34708	oxidoreductase, sh	212	2	SL3413
451	51.8	25	2	S12612	adenomatous polyo	212	2	B70790
452	51.8	29	2	T17079	transmembrane prot	212	2	A44033
453	51.8	31	2	B42176	ALR protein - huma	212	2	SL3413
454	51.8	59	2	A43601	ALR protein - huma	212	2	B70790
455	51.8	63	2	T52277	probable membrane	212	2	A44033
456	51.8	63	2	G92064	oxidoreductase, sh	212	2	SL3413
457	51.8	247	2	S12612	probable membrane	212	2	B70790
458	51.8	64	2	S75543	probable membrane	212	2	A44033
459	51.8	98	2	G91248	probable membrane	212	2	SL3413
460	51.8	101	2	B84708	probable membrane	212	2	B70790
461	51.8	105	2	C87324	platelet-derived g	212	2	A44033
462	51.8	107	2	A64643	hypothetical prote	212	2	SL3413
463	51.8	107	2	C72623	hypothetical prote	212	2	B70790
464	51.8	111	2	C72514	hypothetical prote	212	2	A44033
465	51.8	114	2	H81960	hypothetical inner	212	2	SL3413
466	51.8	115	2	A81017	conserved hypothet	212	2	B70790
467	51.8	127	2	F70910	hypothetical prote	212	2	A44033

541	29	51.8	A12144	probable oxidoreductase
542	29	51.8	I5208	hypothetical prote
543	29	51.8	TVB2A	glycoprotein D - h
544	29	51.8	AG0799	cysteine kinase II (
545	29	51.8	T26339	probable transcript
546	29	51.8	A55111	hypothetical prote
547	29	51.8	JC7638	transcription fact
548	29	51.8	OXP5DA	upstream stimulato
549	29	51.8	T11794	D-amino-acid oxida
550	29	51.8	353	NADH2 dehydrogenas
551	29	51.8	T35531	rieske iron-sulfur
552	29	51.8	B3619	hypothetical prote
553	29	51.8	G71803	neuropeptide Y rec
554	29	51.8	A42565	probable SAM depen
555	29	51.8	369	interleukin-2 rece
556	29	51.8	H69291	conserved hypothet
557	29	51.8	A86364	protein F3F19.3 [1
558	29	51.8	373	interleukin-2 rece
559	29	51.8	T28024	DNA-binding respon
560	29	51.8	T52356	hypothetical prote
561	29	51.8	AB1796	probable SAM depen
562	29	51.8	AH1421	oligogalacturonide
563	29	51.8	D8311	efflux protein hom
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566	29	51.8	400	hypothetical prote
567	29	51.8	402	related to GTP-bin
568	29	51.8	AC2579	tryptophan synthas
569	29	51.8	AF0240	xmt-8b - African
570	29	51.8	T46988	imidazolonepropion
571	29	51.8	G96497	hypothetical prote
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574	29	51.8	406	xmt-8b - African
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577	29	51.8	C75587	flagellum-specific
578	29	51.8	T11319	probable chalcone
579	29	51.8	440	NADH2 dehydrogenas
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583	29	51.8	S33033	virulence ATPase
584	29	51.8	D84451	hypothetical prote
585	29	51.8	T39571	asparagine synthas
586	29	51.8	C86215	probable regulator
587	29	51.8	T43326	protein T6D2.12 [
588	29	51.8	T18805	hypothetical prote
589	29	51.8	D84511	hypothetical prote
590	29	51.8	H69153	probable synthas
591	29	51.8	T39571	protein kinase clk
592	29	51.8	S70352	probable regulator
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594	29	51.8	D69382	hypothetical prote
595	29	51.8	A49367	probable lypY1-TRN
596	29	51.8	D75540	conserved hypothet
597	29	51.8	T39571	probable glycoenz
598	29	51.8	T51430	dolichyl-phosphate
599	29	51.8	H70596	probable protein-k
600	29	51.8	F97546	conserved hypothet
601	29	51.8	T22375	probable lypY1-TRN
602	29	51.8	A86338	conserved hypothet
603	29	51.8	D82063	probable thiamin A
604	29	51.8	537	hypothetical prote
605	29	51.8	AB2266	sulfate permease [
606	29	51.8	S78089	acetylgerophospho
607	29	51.8	A49367	Asn bifunctional p
608	29	51.8	D75540	hypothetical prote
609	29	51.8	T20709	(N-acetyleneuraminy
610	29	51.8	A44128	carboxylesterase [
611	29	51.8	T34842	probable transfe
612	29	51.8	T00445	reverse transcript
613	29	51.8	JC7629	membrane-type fiz
614	29	51.8	T50103	probable oxidoreduc
615	29	51.8	E70930	hypothetical prote
616	29	51.8	A34344	poly (3-hydroxybuty
617	29	51.8	AG0196	protein kinase DYR
618	29	51.8	A82381	conserved hypothet
619	29	51.8	I36231	S-laminin - human
620	29	51.8	A61086	dopamine beta-mono
621	29	51.8	JC134	dopamine beta-mono
622	29	51.8	T40772	protein kinase DYR
623	29	51.8	JG0195	hypothetical prote
624	29	51.8	T20037	metalloprotease
625	29	51.8	S61435	hypothetical prote
626	29	51.8	T37923	hypothetical prote
627	29	51.8	TNB70	BPf-1 protein - pa
628	29	51.8	S63587	two-component sens
629	29	51.8	B84018	hypothetical prote
630	29	51.8	T41120	conserved hypothet
631	29	51.8	S21912	metalloprotease
632	29	51.8	T37923	hypothetical prote
633	29	51.8	S63036	BPf-1 protein - pa
634	29	51.8	T21911	BRCore-TNT1-Q1-Z1
635	29	51.8	T40772	probable translati
636	29	51.8	S21913	conserved hypothet
637	29	51.8	T40772	hypothetical prote
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687	29	51.8	1970	2	T03284	suppressor of ion	
688	29	51.8	2139	2	S46404	keratin high-sulfu	
689	29	51.8	2175	1	S03170	high-sulfur wool m	
690	29	51.8	2201	1	A54774	hypothetical prote	
691	29	51.8	3341	1	A42996	ATP binding caset	
692	29	51.8	3947	2	T02486	genome polyprotein	
693	28	50.9	230	2	T49555	ferrichrome sidero	
694	28	50.9	276	2	T30594	related to high cy	
695	28	50.9	327	2	D86477	conserved hypothet	
696	28	50.9	405	2	H71984	probable RING zinc	
697	28	50.9	415	2	S32932	probable carboxylo	
698	28	50.9	497	2	S22708	regulatory protein	
699	28	50.9	555	2	A60924	homocysteic protein e	
700	28	50.9	1310	1	F86062	perforin 1 Precurs	
701	28	50.9	32	2	E91216	proline dehydrogen	
702	28	50.9	60	2	A30160	alpha-conotoxin Pn	
703	28	50.9	32	1	LPECI	ilvgMDA leader pep	
704	28	50.9	32	2	D87422	ilvgMDA operon le	
710	28	50.9	83	1	N7SR10	ilvgMDA operon le	
711	28	50.9	88	2	H30010	hypothetical ORF-9	
712	28	50.9	89	2	S72603	hypothetical prote	
713	28	50.9	90	2	B75304	H+-transporting tw	
714	28	50.9	63	2	T41452	probable protein t	
715	28	50.9	71	2	D87422	hypothetical prote	
716	28	50.9	99	2	B97574	neurotoxin I', prec	
717	28	50.9	101	2	A97413	hypothetical prote	
718	28	50.9	102	2	A12630	conserved hypothet	
719	28	50.9	106	2	I00722	hypothetical prote	
720	28	50.9	110	2	H96602	virulence-associat	
721	28	50.9	110	2	B72730	hypothetical prote	
722	28	50.9	113	2	A83631	hypothetical prote	
723	28	50.9	118	2	B72524	hypothetical prote	
724	28	50.9	118	2	P72499	conserved hypothet	
725	28	50.9	122	2	JC6548	hypothetical prote	
726	28	50.9	122	2	T46369	unknown protein F1	
727	28	50.9	127	2	B84225	hypothetical prote	
728	28	50.9	129	2	H75351	conserved hypothet	
729	28	50.9	131	2	G32684	hypothetical prote	
730	28	50.9	135	2	C98020	cytidine deaminase	
731	28	50.9	142	2	S06620	high sulfur horn	
732	28	50.9	142	2	T03895	hypothetical prote	
733	28	50.9	143	1	A60159	interleukin-3 prec	
734	28	50.9	144	2	B82423	thioredoxin 2 VCA0	
735	28	50.9	146	2	F90337	hypothetical prote	
736	28	50.9	147	2	I50994	gonaotropin II be	
737	28	50.9	150	2	JCL072	10k zein protein -	
738	28	50.9	152	1	B24427	interleukin-3 prec	
739	28	50.9	152	1	KRSHHHC	keratin high-sulfu	
740	28	50.9	152	2	I47111	high-sulfur wool m	
741	28	50.9	152	2	I47109	high-sulfur wool m	
742	28	50.9	152	2	I47108	seed allergen RAS	
743	28	50.9	152	2	I47112	high-sulfur wool m	
744	28	50.9	158	2	E39925	hypothetical prote	
745	28	50.9	158	2	G71369	ribosomal protein	
751	28	50.9	160	2	S47021	probable quinolone	
752	28	50.9	161	2	T26469	hypothetical prote	
753	28	50.9	161	2	D82799	DNAJ protein homol	
754	28	50.9	162	2	T11855	hypothetical prote	
755	28	50.9	163	2	I47107	seed allergen RAS	
756	28	50.9	166	2	D5299	conserved hypothet	
757	28	50.9	168	2	A6557	nucleoside-diphosp	
758	28	50.9	169	1	OEBCA1	crossover junction	
759	28	50.9	169	2	H85622	cell division inhi	
169	28	50.0	172	1	B90759	hypothetical prote	
169	28	50.0	172	2	KRSHHAA	hypothetical prote	
169	28	50.0	172	2	A71056	hypothetical prote	
169	28	50.0	173	2	B83504	hypothetical prote	
169	28	50.0	174	2	T01486	hypothetical prote	
169	28	50.0	174	2	T49821	hypothetical prote	
169	28	50.0	175	2	T34895	transforming prote	
169	28	50.0	178	1	TVRTEB1	ribosomal-protein-	
169	28	50.0	178	2	A63499	probable ribosomal	
169	28	50.0	180	2	S75415	keratin high-sulfu	
169	28	50.0	181	2	RHRTECE	keratin high-sulfu	
169	28	50.0	182	1	I47105	mannose-binding le	
169	28	50.0	182	2	S62650	hypothetical prote	
169	28	50.0	183	2	F84684	mannitol operon re	
169	28	50.0	184	2	AG0976	hypothetical prote	
169	28	50.0	184	2	H75334	laminin B1 chain v	
169	28	50.0	185	2	A72528	chitin synthase (E	
169	28	50.0	187	1	AF2530	PS2 protein - Rhi	
169	28	50.0	190	2	F65137	hypothetical 21.7	
169	28	50.0	195	2	C75490	tumor necrosis fac	
169	28	50.0	196	2	T31289	wound-inducible ch	
169	28	50.0	197	2	A87286	alkylmercury lyase	
169	28	50.0	198	2	C98302	arylesterase (AF04	
169	28	50.0	199	2	A45067	arylesterase (imp	
169	28	50.0	200	2	AB2981	placental lactogen	
169	28	50.0	201	2	H75599	probable acetyltra	
169	28	50.0	204	1	T23829	deoxyriboe-phosph	
169	28	50.0	205	2	E33985	conserved transcript	
169	28	50.0	205	2	T32135	conserved hypothet	
169	28	50.0	209	2	F91210	hypothetical prote	
169	28	50.0	210	2	A26489	hypothetical prote	
169	28	50.0	212	2	G87629	hypothetical prote	
169	28	50.0	222	2	E83615	heme exporter prot	
169	28	50.0	223	2	A82139	porphobilinogen de	
169	28	50.0	223	2	F91210	hypothetical prote	
169	28	50.0	224	2	A25951	2-hydroxy-6-oxo-2-	
169	28	50.0	224	2	AG3288	hypothetical prote	
169	28	50.0	224	2	B87629	sperm outer dense	
169	28	50.0	224	2	G83462	hypothetical prote	
169	28	50.0	224	2	E86497	outer dense fiber	
169	28	50.0	224	2	B72126	water channel prot	
169	28	50.0	224	2	C75367	C/EBP related prot	
169	28	50.0	224	2	B86023	outer dense fiber	
169	28	50.0	225	2	S71522	hypothetical prote	
169	28	50.0	225	2	C97437	hypothetical prote	
169	28	50.0	225	2	A43905	conserved hypothet	
169	28	50.0	225	2	B82791	hypothetical prote	
169	28	50.0	225	2	I48699	hypothetical prote	
169	28	50.0	226	2	T48885	hypothetical prote	
169	28	50.0	226	2	A37280	hypothetical prote	
169	28	50.0	226	2	D86023	hypothetical prote	
169	28	50.0	226	2	S56100	hypothetical prote	
169	28	50.0	226	2	A71059	hypothetical prote	
169	28	50.0	226	2	JQ1665	transcription init	
169	28	50.0	226	2	AG2554	hypothetical prote	
169	28	50.0	226	2	T04405	hypothetical prote	
169	28	50.0	226	2	GP14-b	14-3-3b protein -	
169	28	50.0	226	2	T04152	outer dense fiber	
169	28	50.0	226	2	C64442	outer dense fiber	
169	28	50.0	226	2	S56101	psA protein - Rhi	
169	28	50.0	226	2	T10535	conserved hypothet	
169	28	50.0	226	2	B83284	hypothetical prote	
169	28	50.0	226	2	AC0564	probable enoyl-coa	
169	28	50.0	226	2	B83045	conserved hypothet	
169	28	50.0	226	2	I50535	hypothetical prote	
169	28	50.0	226	2	D70569	probable lipf prot	

833	28	50.0	279	1	I40494	906	28	50.0	403	2	S28144
834	28	50.0	279	2	SYBBT	907	28	50.0	403	2	S28144
835	28	50.0	279	2	A97871	908	28	50.0	404	2	F82092
836	28	50.0	279	2	H71650	909	28	50.0	410	2	AH2194
837	28	50.0	283	2	G01936	910	28	50.0	410	2	S76984
838	28	50.0	287	2	AH3492	911	28	50.0	413	2	F98155
839	28	50.0	287	2	S71548	912	28	50.0	413	2	AE1132
840	28	50.0	292	2	A60547	913	28	50.0	414	2	AB2242
841	28	50.0	296	2	C49339	914	28	50.0	415	2	F91209
842	28	50.0	297	2	B70994	915	28	50.0	415	2	A88056
843	28	50.0	299	2	A43953	916	28	50.0	415	2	A39412
844	28	50.0	299	2	S08242	917	28	50.0	415	2	BB1281
845	28	50.0	305	1	S52924	918	28	50.0	417	1	WMBEHA
846	28	50.0	305	2	H8334	919	28	50.0	419	2	T10652
847	28	50.0	308	2	AB1957	920	28	50.0	420	2	T4646
848	28	50.0	308	2	JC2253	921	28	50.0	421	2	DB1374
849	28	50.0	309	2	AG0368	922	28	50.0	423	2	A33395
850	28	50.0	310	1	QQBE28	923	28	50.0	425	2	GB3969
851	28	50.0	310	2	T31125	924	28	50.0	425	2	AC2756
852	28	50.0	311	2	H82144	925	28	50.0	426	1	BVBC1D
853	28	50.0	317	2	AI1847	926	28	50.0	429	2	F7784
854	28	50.0	318	2	S14448	927	28	50.0	429	2	T21113
855	28	50.0	319	2	JC2252	928	28	50.0	432	2	AF0567
856	28	50.0	320	2	T30994	929	28	50.0	433	2	B64603
857	28	50.0	322	2	S54806	930	28	50.0	433	2	AT1912
863	28	50.0	330	2	S5953	931	28	50.0	435	2	HB83307
864	28	50.0	322	2	T03614	932	28	50.0	439	2	AF0511
865	28	50.0	323	2	T44728	933	28	50.0	439	2	AD6769
866	28	50.0	324	2	B25102	934	28	50.0	439	2	C99685
867	28	50.0	327	2	D87645	935	28	50.0	439	2	GB5335
868	28	50.0	328	2	T50104	936	28	50.0	439	2	JQ0007
870	28	50.0	330	2	CB2184	937	28	50.0	442	2	AI0121
871	28	50.0	335	2	B45511	938	28	50.0	442	2	CB8232
872	28	50.0	336	1	S18750	939	28	50.0	443	2	JC4067
873	28	50.0	336	2	D69496	940	28	50.0	444	2	C75428
874	28	50.0	340	2	S74712	941	28	50.0	445	2	T44482
875	28	50.0	340	2	S48030	942	28	50.0	447	2	T22163
876	28	50.0	340	2	T14010	943	28	50.0	447	2	T35519
877	28	50.0	341	2	B86503	944	28	50.0	452	2	G86170
878	28	50.0	342	2	H86007	945	28	50.0	454	2	F90875
879	28	50.0	342	2	T19196	946	28	50.0	457	2	B89216
880	28	50.0	342	2	S23438	947	28	50.0	462	2	B81551
881	28	50.0	343	2	G91161	948	28	50.0	462	2	H95914
882	28	50.0	344	2	P90500	949	28	50.0	464	2	B64173
883	28	50.0	345	2	A82448	950	28	50.0	464	2	F96834
884	28	50.0	342	2	AB1376	951	28	50.0	465	2	HB83347
885	28	50.0	350	2	T29436	952	28	50.0	467	2	B72119
886	28	50.0	354	2	T14380	953	28	50.0	469	2	GB1513
887	28	50.0	356	2	A25918	954	28	50.0	470	2	S47892
888	28	50.0	362	2	T17198	955	28	50.0	471	2	T44019
889	28	50.0	363	2	T2254	956	28	50.0	476	2	B95547
890	28	50.0	364	2	AB1333	957	28	50.0	476	2	HB83347
891	28	50.0	376	1	KIBERK	963	28	50.0	483	2	AG1898
892	28	50.0	376	2	C39164	964	28	50.0	487	2	G71432
893	28	50.0	373	2	T40602	965	28	50.0	489	2	AG3038
894	28	50.0	378	2	F6465	966	28	50.0	490	2	D98247
895	28	50.0	387	2	A12152	967	28	50.0	496	2	TA21079
896	28	50.0	387	2	T02780	968	28	50.0	496	2	C87194
897	28	50.0	388	2	DB1882	969	28	50.0	498	2	AC1930
898	28	50.0	388	2	F81137	970	28	50.0	513	2	T37180
899	28	50.0	388	2	JQ0189	971	28	50.0	515	2	T47257
900	28	50.0	391	2	S49100	972	28	50.0	505	2	T03354
901	28	50.0	392	2	C83151	973	28	50.0	529	2	AH1463
902	28	50.0	394	2	JC1420	974	28	50.0	532	1	WB2BFB5
903	28	50.0	396	2	A97562	975	28	50.0	536	2	T2626
904	28	50.0	397	2	S71339	976	28	50.0	537	2	B81734
905	28	50.0	401	2	A75388	977	28	50.0	537	2	H71471

hypothetical prote  
neuroglycan C pre  
hypothetical prote  
hypothetical prote  
transcription fact  
pol polyprotein -  
DNA polymerase III  
hypothetical prote  
hypothetical prote  
phosphoprotein pho  
hypothetical prote  
conserved hypothet  
NADH2 dehydrogenas  
probable 3,4-dihyd  
hypothetical prote  
NADH2 dehydrogenas  
hypothetical prote  
glucan 1,-alpha-g  
gene 28 protein -  
hypothetical prote  
membrane transloca  
protein C43E11.8 [

979 28 50.0 538 2 E72752  
980 28 50.0 544 2 I55454  
981 28 50.0 548 2 A75357  
982 28 50.0 554 2 D72760  
983 28 50.0 559 2 S54358  
984 28 50.0 559 2 A46311  
985 28 50.0 565 2 G89813  
986 28 50.0 567 2 A86262  
987 28 50.0 570 2 D72597  
988 28 50.0 577 2 B44307  
989 28 50.0 578 2 T41715  
990 28 50.0 590 2 A82350  
991 28 50.0 591 2 S14115  
992 28 50.0 594 2 T06369  
993 28 50.0 599 2 T15552  
994 28 50.0 615 2 S77332  
995 28 50.0 615 2 T34392  
996 28 50.0 616 2 S33908  
997 28 50.0 620 2 W2BBC1  
998 28 50.0 622 2 B96751  
999 28 50.0 629 2 E47096  
1000 28 50.0 630 2 GB7753

## ALIGNMENTS

## RESULT 1

YXMSST

thymidylate synthase (EC 2.1.1.45) - mouse

C; Species: Mus musculus (house mouse)

C; Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 05-Oct-2004

C; Accession: A26323; A24157; 148858

R; Deng, T.; Li, D.; Jenh, C.H.; Johnson, L.F.

J. Biol. Chem. 261, 16000-16005, 1986

A; Title: Sequence of a cDNA for mouse thymidylate synthase. Locations of introns and

A; Reference number: A24157; PMID:88174353; PMID:3782103

A; Accession: A26323

A; Molecule type: DNA

A; Residues: 1-307 &lt;DNA&gt;

A; Cross-references: UNIPARC:UPI0000003FEE; GB:M13352; PIDN:9202048; PIDN:

R; Perryman, S.M.; Rossana, C.; Deng, T.; Vanin, E.F.; Johnson, L.F.

Mol. Biol. Evol. 3, 313-321, 1986

A; Title: Sequence of a cDNA for mouse thymidylate synthase reveals striking similarity w

A; Reference number: A24157; PMID:88174353; PMID:3444407

A; Accession: A24157

A; Molecule type: mRNA

A; Residues: 1-307 &lt;PER&gt;

A; Cross-references: UNIPARC:UPI0000003FEE; GB:M13019; PIDN:AAA40439.1; PID:

R; Deng, T.L.; Li, Y.; Johnson, L.F.

Proc. Natl. Acad. Sci. U.S.A. 86, 65-68, 1989

A; Title: Thymidylate synthase gene expression is stimulated by some (but not all) intron

A; Reference number: I48858; MUID:89128436; PMID:2915925

A; Accession: I48858

A; Status: translated from GB/EMBL/DBJ

A; Molecule type: mRNA

A; Residues: 236-265 &lt;RES&gt;

A; Cross-references: UNIPARC:UPI00016D097; ENBL:X14489; PIDN:954931; PIDN:CRA32651.1; PID:

C; Genetics

A; Intron: 63/1; 87/3; 146/1; 180/1; 238/3; 262/3

C; Superfamily: thymidylate synthase; thymidylate synthase homology

C; Keywords: deoxyribonucleotide biosynthesis; methyltransferase

F; 24-307/Domain: thymidylate synthase homology &lt;TDS&gt;

F; 193/Active site: CyB #status predicted

A; Query Match

Best Local Similarity 100.0%; Pred. No. 0.018%; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 LMALPPCHAL 10

Db 183 LMALPPCHAL 192

hypothetical prote  
neuroglycan C pre  
hypothetical prote  
hypothetical prote  
transcription fact  
pol polyprotein -  
DNA polymerase III  
hypothetical prote  
hypothetical prote  
hypothetical prote  
phosphoprotein pho  
hypothetical prote  
hypothetical prote  
conserved hypothet  
NADH2 dehydrogenas  
probable 3,4-dihyd  
hypothetical prote  
NADH2 dehydrogenas  
hypothetical prote  
glucan 1,-alpha-g  
gene 28 protein -  
hypothetical prote  
membrane transloca  
protein C43E11.8 [

979 28 50.0 538 2 E72752  
980 28 50.0 544 2 I55454  
981 28 50.0 548 2 A75357  
982 28 50.0 554 2 D72760  
983 28 50.0 559 2 S54358  
984 28 50.0 559 2 A46311  
985 28 50.0 565 2 G89813  
986 28 50.0 567 2 A86262  
987 28 50.0 570 2 D72597  
988 28 50.0 577 2 B44307  
989 28 50.0 578 2 T41715  
990 28 50.0 590 2 A82350  
991 28 50.0 591 2 S14115  
992 28 50.0 594 2 T06369  
993 28 50.0 599 2 T15552  
994 28 50.0 615 2 S77332  
995 28 50.0 615 2 T34392  
996 28 50.0 616 2 S33908  
997 28 50.0 620 2 W2BBC1  
998 28 50.0 622 2 B96751  
999 28 50.0 629 2 E47096  
1000 28 50.0 630 2 GB7753

## RESULT 2

thymidylate synthase (EC 2.1.1.45) - rat

C; Species: Rattus norvegicus (Norway rat)

C; Date: 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C; Accession: S53715

R; Ciesla, J.; Weiner, K.X.B.; Reston, J.T.; Maley, G.F.; Maley, F.

Biochim. Biophys. Acta 1261, 233-242, 1995

A; Title: Isolation and expression of rat thymidylate synthase cDNA: Phylogenetic compar

A; Reference number: S53715; MUID:95226650; PMID:7711067

A; Accession: S53715

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-307 <CIE>

A; Cross-references: UNIPROT:P45352; UNIPARC:UPI0000112C76; EMBL:L12138; NID:9207327; PID:

C; Superfamily: thymidylate synthase; thymidylate synthase homology

C; Keywords: methyltransferase

F; 24-307/Domain: thymidylate synthase homology <TDS>

Query Match 100.0%; Score 56; DB 2; Length 307;

Best Local Similarity 100.0%; Pred. No. 0.018%; Indels 0; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 LMALPPCHAL 10

Db 183 LMALPPCHAL 192

## RESULT 3

YXHUT

thymidylate synthase synthase (EC 2.1.1.45) - human

C; Species: Homo sapiens (man)

C; Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 05-Oct-2004

C; Accession: A23047; I55318; JU0120; A22393; A33442

R; Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.

J. Biol. Chem. 265, 575-583, 1990

A; Title: Structural and Functional Analysis of the Human Thymidylate Synthase Gene.

A; Reference number: I55318; PMID:1056070; PMID:2243092

A; Accession: I55318

A; Status: translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-313 <RES>

A; Cross-references: UNIPARC:UPI0000001225; GB:D00596; PIDN:9220135; PIDN:937478; PIDN:X02308; PIDN:937478

R; Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.

J. Biol. Chem. 265, 575-583, 1990

A; Title: Human thymidylate synthase gene: isolation of phage clones which cover a functi

A; Reference number: JU0120; MUID:901051; PMID:2532645

A; Accession: JU0120

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-313 <RES>

A; Cross-references: UNIPARC:UPI0000001225; GB:D00596; PIDN:9220135; PIDN:937478; PIDN:X02308; PIDN:937478

R; Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.

J. Biol. Chem. 265, 575-583, 1990

A; Title: Purification and NH2-terminal amino acid sequence of human thymidylate synthase

A; Reference number: A22393; MUID:8526174; PMID:3839505

A; Accession: A22393

A; Status: protein

A; Residues: 2-25 <SHI>

A; Cross-references: UNIPARC:UPI00001722FF

R; Davission, V.J.; Sirawaraporn, W.; Santu, D.V.

J. Biol. Chem. 264, 9145-9148, 1989

A; Title: Expression of human thymidylate synthase in Escherichia coli.

A; Reference number: A338432; MUID:89255101; PMID:2656695

A;Accession: A33842  
A;Molecule type: protein  
A;Residues: 2-10 <DAYS  
A;Cross-references: UNIPARC:UPI00001722FF  
C;Genetics:  
A;Gene: GDB:TYMS  
A;Cross-references: GDB:120465; OMIM:188350  
A;Inton position: 18p11.32-18p11.32  
A;Intron: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3  
C;Superfamily: thymidylate synthase; thymidylate synthase homology  
C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase  
P;30-313/Domain: thymidylate synthase homology <TDS>  
P;199/Active site: Cys #status predicted

Query Match 100.0%; Score 56; DB 1; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.018; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALPPCHAL 10  
Db 189 MALPPCHAL 198

RESULTS 4  
G81050  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.; Hickie, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.  
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A;Reference number: A81000; PMID:20175755; PMID:10710307  
A;Accession: G81050  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-264 <TT>  
A;Cross-references: UNIPROT:Q9JY72; UNIPARC:UPI00001378E6; GB:AE002521; GB:AE002098; NID  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB1709  
C;Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 100.0%; Score 56; DB 1; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.018; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALPPCHAL 10  
Db 141 MALPPCHAL 149

RESULTS 5  
A81825  
C;Species: *Neisseria meningitidis*  
C;Accession: A81825  
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A;Reference number: A81775; PMID:2022556; PMID:10761919  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-264 <PAR>  
A;Cross-references: UNIPROT:Q9JY75; UNIPARC:UPI00001378E5; GB:AL162757; GB:AL157959; NID  
C;Genetics:

Db 191 MALPPCHSL 199

RESULT 8

AB1681 thymidylate synthase homolog lin1988 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Accession: AB1681 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 05-Oct-2004 C;Cross-references: UNIPROT:Q92AD4; UNIPARC:UPI00001378D6; GB:AL592022; PID:9328774; PMID:8510640 A;Title: Comparative genomics of Listeria species. A;Authors: Kretter, T.; Simoes, N.; J. Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001. A;Residues: 1-114 <GLA> A;Cross-references: UNIPROT:Q92AD4; UNIPARC:UPI00001378D6; GB:AL592022; PID:9328774; PMID:8510640 A;Experimental source: strain Clip11262 C;Genetics: A;Status: preliminary C;Superfamily: thymidylate synthase; thymidylate synthase homology Query Match Score 49; DB 2; Length 314; Best Local Similarity 88.9%; Pred. No. 0.3%; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Db 191 MALPPCHSL 199

RESULT 9

CT0881 probable thyA protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Accession: CT0881 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 05-Oct-2004 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skilton, S.; Squares, S. Nature 393, 537-544, 1998. A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:3634230 A;Accession: CT0881 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-263 <COL> A;Cross-references: UNIPROT:O33306; UNIPARC:UPI00001378E3; GB:AL008967; GB:AL123456; PMID:98295987; PMID:11743193 C;Genetics: A;Gene: thyA C;Superfamily: thymidylate synthase homology <TDS> Query Match Score 48; DB 2; Length 263; Best Local Similarity 100.0%; Pred. No. 0.39%; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 141 MALPPCHA 9

RESULT 10

S35239 thymidylate synthase (EC 2.1.1.45) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Accession: AB3328 C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 05-Oct-2004 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzari, P.H.; Hagiwara, S.; O'Callaghan, D.; Letessier

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
 A;Reference number: AB2252; PMID:11756688

A;Accession: AB3328  
 A;Species: preliminary

A;Molecule type: DNA  
 A;Residues: 1-264 <KUR>

A;Cross-references: UNIPROT:Q8YI37; UNIPARC:UPI0000057D4A; GB:AB008917; PIDN:AAL51789.1;

A;Experimental source: strain 16M

A;Gene: BMET0608

A;Map position: I

C;Superfamily: thymidylate synthase; thymidylate synthase homology

C;Keywords: methyltransferase

A;Map position: circular chromosome 1  
 C;Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match Score 48; DB 2; Length 264;  
 Best Local Similarity 88.9%; Pred. No. 0.39%; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 141 MALPPCHCL 149

Query Match Score 48; DB 2; Length 264;  
 Best Local Similarity 88.9%; Pred. No. 0.39%; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 156 MALPPCHCL 164

RESULT 13

A87099  
 thymidylate synthase [imported] - *Mycobacterium leprae*

C;Species: *Mycobacterium leprae*

C;Accession: A87099

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 05-Oct-2004

R;Cole, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hoyle, R.; Davies, R.M.; Devlin, K.; Dutfoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus

A;Number: A46909; MUID:21128732; PMID:11224002

A;Accession: A87099

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <STO>

A;Cross-references: UNIPROT:Q9CBW0; UNIPARC:UPI00001378E0; GB:AL450380; NID:91309353; F

C;Genetics:

A;Gene: thyA

C;Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match Score 48; DB 2; Length 266;

Best Local Similarity 100.0%; Pred. No. 0.39%; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHA 9

Db 144 MALPPCHA 151

RESULT 14

G57605  
 hypothetical protein AGR\_C\_3709 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium\_tumefaciens

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, P.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2329, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A;Number: A97359; MUID:21608551; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-279 <KUR>

A;Cross-references: UNIPARC:UPI00001643BB; GB:AE007869; PIDN:AAK87800.1; PMID:91515774;

C;Genetics:

A;Gene: AGR\_C\_3709

Query Match Score 48; DB 1; Length 290;

Best Local Similarity 88.9%; Pred. No. 0.42%; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 167 MALPPCHCL 175

RESULT 17  
 T42984

thymidylate synthase (EC 2.1.1.45) - ateline herpesvirus 3 (strain 73)  
 C;Species: ateline herpesvirus 3  
 C;Variety: strain 73  
 C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C;Accession: TA2984  
 R;Albrecht, J.C.; Fleckenstein, B.  
 A;Description: Primary structure of the herpesvirus atelies genome.  
 A;Reference number: 222274  
 A;Accession: TA2984  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-250 <DNA>  
 A;Cross-references: UNIPROT:Q9YTJ6; UNIPARC:UPI0000F8B14; EMBL:AF083424; PIDN: AAC95595.  
 A;Experimental source: strain 73  
 C;Superfamily: thymidylate synthase; thymidylate synthase homology  
 C;Keywords: methyltransferase

Query Match      85.7%;    Score 48;    DB 2;    Length 290;  
 Best Local Similarity    88.9%;    Pred. No. 0.42;    Indels 0;    Gaps 0;

Qy      2 MALPPCHAL 10  
 Db      167 MALPPCHVL 175

## RESULT 18

SYBB13  
 thymidylate synthase (EC 2.1.1.45) - human herpesvirus 3  
 C;Species: human herpesvirus 3, varicella-zoster virus  
 C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Oct-2004  
 C;Accession: D27342  
 R;Davidson, A.J.; Scott, J.B.  
 J. Gen. Virol. 67, 1759-1816, 1986  
 A;Title: The complete DNA sequence of varicella-zoster virus.  
 A;Reference number: A27345; MUID:86306657; PMID:3018124  
 A;Accession: D27342  
 A;Molecule type: DNA  
 A;Residues: 1-301 <DNA>  
 A;Cross-references: UNIPROT:PO9249; UNIPARC:UPI00001378F0; EMBL:X04370; PIDN:959989;

C;Genetics:  
 A;Gene: 13

C;Superfamily: thymidylate synthase; thymidylate synthase homology

F;18-301/Domain: thymidylate synthase homology; methyltransferase  
 F;183/Active site: Cys #status predicted  
 Query Match      85.7%;    Score 48;    DB 1;    Length 301;  
 Best Local Similarity    80.0%;    Pred. No. 0.44;    Indels 0;    Gaps 0;

Qy      1 LMALPPCH 8  
 Db      177 LMVLPPECHL 186

RESULT 19  
 SYLBT  
 thymidylate synthase (EC 2.1.1.45) - Lactobacillus casei

C;Species: Lactobacillus casei  
 C;Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 05-Oct-2004  
 C;Accession: A29817; A00548  
 R;Pinter, K.; Davison, V.J.; Santi, D.V.  
 DNA 7, 235-241, 1988  
 A;Title: Cloning, sequencing, and expression of the Lactobacillus casei thymidylate synthase gene. Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A29817; MUID:88283342; PMID:2840247  
 A;Accession: A29817  
 A;Molecule type: DNA  
 A;Residues: 1-316 <DNA>  
 A;Cross-references: UNIPROT:PO0469; UNIPARC:UPI00001123C7; GB:M19653  
 R;Maley, G.P.; Bellisario, R.L.; Guarino, D.U.; Maley, F.  
 J. Biol. Chem. 254, 1301-1304, 1979

A;Title: The primary structure of *Lactobacillus casei* thymidylate synthetase. III. The ultimate amino acid sequence of the enzyme.  
 A;Reference number: A00548; MUID:7910913; PMID:105005  
 A;Accession: A00548  
 A;Molecule type: protein  
 A;Residues: 1-316 <DNA>  
 A;Cross-references: UNIPARC:UPI00001123C7  
 A;Note: This is the final paper of a series  
 C;Superfamily: thymidylate synthases; thymidylate synthase homology  
 C;Keywords: deoxyribonucleotide biosynthesis; homodimer; methyltransferase  
 F;3-316/Domain: thymidylate synthase homology <DB>  
 F;198/Active site: Cys #status experimental

Query Match      85.7%;    Score 48;    DB 1;    Length 316;  
 Best Local Similarity    88.9%;    Pred. No. 0.46;    Indels 0;    Gaps 0;  
 Matches 8;    Conservative 0;    Mismatches 1;    Indels 0;    Gaps 0;  
 Qy      2 MALPPCHAL 10  
 Db      193 LMALPPCHL 201

## RESULT 20

T05277  
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Arabidopsis thaliana (mouse-ear cress)  
 N;Alternate names: protein T4L20\_150  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 31-Dec-2004  
 C;Accession: T05277  
 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysschaert, C.; Dasbasseville, R.; De Clerck, R.; Dewes, H.W.; Mayer, K.F.X.; Schueler, C.; submitted to the Protein Sequence Database, September 1998  
 A;Reference number: Z15406  
 A;Accession: T05277  
 A;Molecule type: DNA  
 A;Residues: 1-318 <BEV>  
 A;Cross-references: UNIPROT:Q005763; UNIPARC:UPI000000BF1C; EMBL:AL023094  
 A;Experimental source: cultivar Columbia; BAC clone T4L20  
 C;Genetics:  
 A;Map position: 4  
 A;Introns: 138/2; 267/3; 282/3; 304/3; 325/2; 350/2; 447/1; 482/3  
 A;Note: T4L20\_150  
 C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate synthase  
 C;Keywords: methyltransferase NADP; oxidoreductase  
 F;19-341/Domain: Type I dihydrofolate reductase homology <DFR>  
 F;235-518/Domain: thymidylate synthase homology <TS>  
 Query Match      85.7%;    Score 48;    DB 2;    Length 518;  
 Best Local Similarity    100.0%;    Pred. No. 0.73;    Indels 0;    Gaps 0;  
 Matches 8;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 Qy      1 LMALPPCH 8  
 Db      394 LMALPPCH 401

## RESULT 21

E84539  
 dihydrofolate reductase-thymidylate synthase [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
 C;Accession: B84539  
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Trallon, L.; Eissner, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosomes 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: B84539  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-519 <STO>  
 A;Cross-references: UNIPARC:UPI0000017CC; GB:AE002093; NID:94544392; PI:

C;Genetics:	
A;Gene: Atg16370	
A;Map position: 2	
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase	thymidylate synthase (EC 2.1.1.45) - carrot
Query Match	85.7%; Score 48; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 0.73;	Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 LMALPPCH 8	
Db 395 LMALPPCH 402	
RESULT 22	
S3.5272	dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - carrot
C;Species: Daucus carota (carrot)	
C;Date: 10-Dec-1993 #sequence_revision 19-Jan-1996 #text_change 31-Dec-2004	
R;Luo, M.; Piffanelli, P.; Rastelli, L.; Cella, R.	
Plant Mol. Biol. 22, 427-435, 1993	
A;Title: Molecular cloning and analysis of a cDNA coding for the bifunctional dihydrofolate reductase/thymidylate synthase	
A;Reference number: S35272; PMID:9320381; PMID:8129682	
A;Accession: S35272	
A;Molecule type: mRNA	
A;Residues: 1-528 <LUO>	
C;Cross-references: UNIPROT:P45350; UNIPARC:UPI0001298A3; EMBL:217306; NID:9288614; PID:217306; NID:9288614	
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase	thymidylate synthase
C;Keywords: methyltransferase; NADP; oxidoreductase	
F;23-146/Domain: type I dihydrofolate reductase homology <DPR>	
F;244-528/Domain: thymidylate synthase homology <TDS>	
Query Match	85.7%; Score 48; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.74;	Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 LMALPPCH 8	
Db 403 LMALPPCH 410	
RESULT 23	
S5.5663	dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - soybean
C;Species: Glycine max (soybean)	
C;Accession: S55663	thymidylate synthase 70 - equine herpesvirus 2
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004	
R;Wang, M.; Ratnam, S.; Preisham, J.H.	
Biochim. Biophys. Acta 1281, 325-336, 1995	
A;Title: Cloning, nucleotide sequence and expression of the bifunctional dihydrofolate reductase/thymidylate synthase	
A;Reference number: S55663; PMID:7742362	
A;Accession: S55663	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-510 <WAN>	
C;Cross-references: UNIPROT:P51820; UNIPARC:UPI0001298A3; GB:S78087; NID:9999189; PID:NID:9999189	
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase	thymidylate synthase
C;Keywords: methyltransferase; NADP; oxidoreductase	
F;26-149/Domain: type I dihydrofolate reductase homology <DPR>	
F;247-530/Domain: thymidylate synthase homology <TDS>	
Query Match	85.7%; Score 48; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.74;	Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 LMALPPCH 8	
Db 406 LMALPPCH 413	
RESULT 24	
S5.5667	thymidylate synthase 70 - equine herpesvirus 2
C;Species: equine herpesvirus 2	
C;Accession: S55667	thymidylate synthase 70 - equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004	
R;Teiford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.	
J. Mol. Biol. 249, 520-528, 1995	
A;Title: The DNA sequence of equine herpesvirus 2	
A;Reference number: S55667	
A;Accession: S55667	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-289 <TEL>	
A;Cross-references: UNIPROT:Q89940; UNIPARC:UPI00001378D2; GB:U20824; NID:9695172; PIDN:9695172	
C;Superfamily: thymidylate synthase; thymidylate synthase homology	
F;6-289/Domain: thymidylate synthase homology <TDS>	
Query Match	83.9%; Score 47; DB 2; Length 289;
Best Local Similarity 88.3%; Pred. No. 0.63;	Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 MALPPCH 10	
Db 166 MALPPCH 174	

**RESULT 26**  
**E75250** thymidylate synthase - Deinococcus radiodurans (strain R1)  
*C;Species: Deinococcus radiodurans*  
*C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 05-Oct-2004*  
**R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.**  
*Science 286, 1571-1577, 1999*  
*A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.*  
*A;Reference number: A75250; MUID:20036896; PMID:10567266*  
*A;Accession: E75250*  
*A;Status: preliminary*  
*A;Molecule type: DNA*  
*A;Residues: 1-387 <WII>*  
*A;Cross-references: UNIPROT:Q9RR67; UNIPARC:UPI00000D3FF9; GB:AE000513; NID:15756*  
*A;Experimental source: strain R1*  
*C;Genetics:*  
*A;Gene: DRA630*  
*A;Map position: 1*  
*C;Superfamily: thymidylate synthase*

Query Match 83.9%; Score 47; DB 2; Length 387;  
 Best Local Similarity 88.9%; Pred. No. 0.83; Mismatches 0; Gaps 0;  
 Matches 8; Conservative 0; Indels 0;

Qy 2 MALPPCHAL 10  
 Db 264 MALPPCHL 272

**RESULT 27**  
**RD1NTS** dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m  
*C;Species: Leishmania major*  
*C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 31-Dec-2004*  
**R;Beverley, S.M.; Ellenberger, T.E.; Cordingley, J.S.**  
*Proc. Natl. Acad. Sci. U.S.A. 83, 2584-2588, 1986*  
*A;Title: Primary structure of the gene encoding the bifunctional dihydrofolate reductase*  
*A;Reference number: A23403; MUID:86205996; PMID:3458220*  
*A;Accession: A23403*  
*A;Molecule type: DNA*  
*A;Residues: 1-520 <BBV>*  
*A;Cross-references: UNIPROT:PO7382; UNIPARC:UPI00001298A5; EMBL:M12734; NID:gi159309; PID:R; Grumont, R.; Washtoni, W.L.; Caput, D.; Santini, D.V.*  
*Proc. Natl. Acad. Sci. U.S.A. 83, 5387-5391, 1986*  
*A;Title: Bifunctional thymidylate synthase-dihydrofolate reductase from Leishmania tropi*  
*A;Reference number: A24311; MUID:86287263; PMID:3461439*  
*A;Accession: A24311*  
*A;Molecule type: DNA*  
*A;Residues: 1-48; 'S', '50-71', 'EEQR', '77-124'; 'RML', '128-305, 'T', '308-396, 'V', '398-520 <GRU>*  
*A;Cross-references: UNIPARC:UPI0000172303; GB:MI14330*  
*R;Garvey, B. P.; Santini, D.V.*  
*Proc. Natl. Acad. Sci. U.S.A. 82, 7188-7192, 1985*  
*A;Title: Limited proteolysis of the bifunctional thymidylate synthase-dihydrofolate redu*  
*A;Reference number: A24734; MUID:86042631; PMID:3903747*  
*A;Accession: A24734*  
*A;Molecule type: Protein*  
*A;Residues: 334-345; 'G', '347,349-352,354-358,360-361 <GAR>*  
*A;Cross-references: UNIPARC:UPI0000172306*  
*C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate synthase; deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme*  
*P;26-166/Domain: type I dihydrofolate reductase homology <DFR>*  
*P;234-520/Domain: thymidylate synthase homology <TS>,*  
*F;400/Active site: Cys #status predicted*

Query Match 83.9%; Score 47; DB 1; Length 583;  
 Best Local Similarity 88.9%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 460 MALPPCHL 468

**RESULT 28**  
**RD1NTZ** dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m  
*C;Species: Leishmania mexicana amazônica*  
*C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 31-Dec-2004*  
**R;Nelson, K.; Alonso, G.; Langer, P.J.; Beverley, S.M.**  
*Nuclic Acids Res. 18, 2819, 1990*  
*A;Title: Sequence of the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene of*  
*A;Reference number: S15756; MUID:30251168; PMID:2339068*  
*A;Accession: S15756*  
*A;Status: translation not shown*  
*A;Molecule type: DNA*  
*A;Residues: 1-520 <NEL>*  
*A;Cross-references: UNIPROT:PI6126; UNIPARC:UPI00001298A4; EMBL:X51735; NID:91470; PIDN:R26-166/Domain: type I dihydrofolate reductase/thymidylate synthase; thymidylate synthase; multifunctional enzyme*  
*C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase; homology <DFR>*  
*F;234-520/Domain: type I dihydrofolate reductase homology <TS>,*  
*F;400/Active site: Cys #status predicted*

Query Match 83.9%; Score 47; DB 1; Length 520;  
 Best Local Similarity 88.9%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 395 MALPPCHL 403

**RESULT 29**  
**RDZQTB** dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium c  
*C;Species: Plasmodium chabaudi*  
*C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 31-Dec-2004*  
*R;Cowman, A.F.; Lew, A.M.*  
*Mol. Cell. Biol. 9, 5182-5188, 1989*  
*A;Title: Antifolate drug selection results in duplication and rearrangement of chromosomal genes*  
*A;Reference number: A33484; MUID:9009735; PMID:2601715*  
*A;Molecule type: DNA*  
*A;Residues: 1-583 <COW>*  
*A;Cross-references: UNIPROT:P20712; UNIPARC:UPI00001298A9; GB:MI0834; NID:9160265; PIDN:R26-164/Domain: type I dihydrofolate reductase/thymidylate synthase; thymidylate synthase; multifunctional enzyme*  
*C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase; homology <DFR>*  
*F;300-583/Domain: thymidylate synthase homology <TS>,*  
*F;465/Active site: Cys #status predicted*

Query Match 83.9%; Score 47; DB 1; Length 583;  
 Best Local Similarity 88.9%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 460 MALPPCHL 468

**RESULT 30**  
**RDZQKL** dihydrofolate reductase (BC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - malaria parasite  
*C;Species: Plasmodium falciparum*  
*C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1993 #text\_change 31-Dec-2004*  
*C;Accession: A3995; A3162; B3162; C31262; F31262; JS0208; D31262*  
*R;Bzik, D.J.; Li, W.; Horii, T.; Inselburg, J.*  
*Proc. Natl. Acad. Sci. U.S.A. 84, 8360-8364, 1987*

A;Title: Molecular cloning and sequence analysis of the Plasmodium falciparum dihydrofolate reductase gene from									
A;Reference: A39975; MUID:8806594; PMID:2825189									
A;Accession: A39875 A;Molecule type: DNA A;Residues: 1-608 <S27> A;Cross-references: UNIPROT:PI13922; UNIPARC:UPI000016BF8B; GB:J03028; NID:9160261; PIDN:R;Cowan,A.F.; Morry, M.J.; Biggs, B.A.; Cross, G.A.M.; Foote, S.J. Proc. Natl. Acad. Sci. U.S.A., 85, 9109-9113, 1988 A;Title: Amino acid changes linked to pyrimethamine resistance in the dihydrofolate reductase gene. A;Reference number: A94216; MUID:89057885; PMID:3057439									
A;Accession: A31262 A;Molecule type: DNA A;Residues: 1-608 <COW1> A;Cross-references: UNIPARC:UPI000016BF8B; GB:J03772; NID:9340507; PIDN:AB592212; PID:R;Cowan,A.F.; Morry, M.J.; Biggs, B.A.; Cross, G.A.M.; Foote, S.J. Proc. Natl. Acad. Sci. U.S.A., 85, 9109-9113, 1988 A;Note: These two sequences are from two different clones, HB3 and 7G8									
A;Accession: G31262 A;Molecule type: DNA A;Residues: 1-15, 'V, '17-107, 'T, '109-608 <COW> A;Cross-references: UNIPARC:UPI0000172307 A;Accession: C31262 A;Molecule type: DNA A;Residues: 1-107, 'S, '109-258 <CO2> A;Cross-references: UNIPARC:UPI0000172307 A;Accession: B31262 A;Molecule type: DNA A;Residues: 1-58, 'R, 60-258 <CO3> A;Cross-references: UNIPARC:UPI0000172307 A;Accession: F31262 A;Molecule type: DNA A;Residues: 1-56, 'R, '60-163, 'L, '165-258 <CO4> A;Cross-references: UNIPARC:UPI0000172307 R;Shawin, V.A.; England, S.M.; Sims, P.R.G.; Hyde, J.B. Gene 76, 41-52, 1989 A;Title: Characterisation of the dihydrofolate reductase-thymidylate synthetase gene from Plasmodium falciparum. A;Reference number: JS0208; MUID:8930658; PMID:2663650									
A;Accession: JS0208 A;Molecule type: DNA A;Residues: 1-58, 'R, 60-608 <SNP> A;Cross-references: UNIPARC:UPI00001298AA; GB:M22159; NID:9160259; PIDN:AAA29580_1; PID:R;Cowan,A.F.; Morry, M.J.; Biggs, B.A.; Cross, G.A.M.; Foote, S.J. A;Experiment source: strain K1 A;Note: the authors suggest that translation may begin at Met-2 A;Note: this sequence is from a pyrimethamine-resistant strain; the sequence from the pyrimethamine-resistant strain is identical to the wild-type sequence except for a single nucleotide change at position 2. The wild-type sequence is identical to the sequence reported by Cowan et al. (1988). C;Comment: Dihydrofolate reductase catalyzes the production of methylenetetrahydrofolate C;Genetics: A;Map position: 4 C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate synthase; thymidylate synthetase; deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme; C;Keywords: F;27-163/F;325-608/Domain: type I dihydrofolate reductase homology <DBR> F;325-608/Domain: thymidylate synthase homology <TDS> F;499/Active site: Cys #status predicted									
Query Match Score 83.9%; Score 47; DB 1; Length 608; Best Local Similarity 88.9%; Pred. No. 1.3; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	2	MLPPCH1	10						
Dy	485	MLPPCH1	493						
RESULT 31 A46005 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Toxoplasma gondii C;Species: Toxoplasma gondii C;Date: 21-Sep-1993 C;Accession: A46005 R;Roos, D. S. J. Biol. Chem. 268, 6269-6280, 1993									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
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A;Title: Primary structure of the dihydrofolate reductase-thymidylate synthase gene from									
A;Title: Primary structure of the dihydrofolate reduct									

C;Genetics: A;Gene: thyA	Qy 2 MALPPCHAL 10 Db 340 MALPPCHVM 348
C;Superfamily: thymidylate synthase; thymidylate synthase homology	
C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase	
P;6-18/Domain: thymidylate synthase homology <TDS>	
P;201/Active site: Cys #status predicted	
RESULT 36	
T09609 uroplakin II - human	
C;Species: Homo sapiens (man)	
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004	
C;Accession: T09609	
R;Smith, B.A.; Lobban, B.D.; Hall, G.D.; Harnden, P.; Selby, P.J.; Trejdoski Am. J. Pathol. 153, 1957-1967, 1998	
A;Title: Uroplakin gene expression by normal and neoplastic human urothelium.	
A;Reference number: Z16771; MUID:99061442; PMID:9846985	
A;Accession: T09609	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: mRNA	
A;Residues: 1-184 <SMI>	
A;Cross-references: UNIPROT:0000526; UNIPARC:UPI0000137CD3; EMBL:Y13645; NID:93493010; PI	
A;Experimental source: ureter	
Query Match Score 46; DB 1; Length 318; Best Local Similarity 77.8%; Pred. No. 1; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy 2 MALPPCHAL 10 Db 196 MALPPCHM 204	
RESULT 34	
C89920 thymidylate synthase [imported] - Staphylococcus aureus (strain N315)	
C;Species: Staphylococcus aureus	
C;Accession: C89920	#sequence_revision 10-May-2001 #text_change 05-Oct-2004
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, M.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	
Lancet 357, 1225-1240, 2001	
A;Title: Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> .	
A;Reference number: A89758; MUID:21311952; PMID:11418146	
A;Accession: C89920	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-18 <KUR>	
A;Cross-references: UNIPROT:Q99U61; UNIPARC:UPI00001378EE; GB:BA000018; PID:g13701225; E	
A;Experimental source: strain N315	
C;Genetics:	
C;Superfamily: thymidylate synthase; thymidylate synthase homology	
Query Match Score 46; DB 2; Length 318; Best Local Similarity 77.8%; Pred. No. 1; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy 2 MALPPCHAL 10 Db 196 MALPPCHM 204	
RESULT 35	
S65570 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Paramaecium t	
C;Species: Paramecium tetraurelia	
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004	
C;Accession: S65570	
R;Schlichtherle, I.M.; Roos, D.S.; van Houten, J.L.	
Mol. Gen. Genet. 250, 665-673, 1996	
A;Title: Cloning and molecular analysis of the bifunctional dihydrofolate reductase/thymidylate synthase/thymidylate synthase synthase; thymidylate synthase by	
A;Reference number: S65570; PMID:8628226	
A;Accession: S65570	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-462 <SCH>	
A;Cross-references: UNIPROT:Q27828; UNIPARC:UPI00001298A7; EMBL:U03885; NID:g134591; PID	
C;Genetic code: SGCS	
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase	
C;Keywords: methytransferase; NADP; oxidoreductase	
P;6-111/Domain: type I dihydrofolate reductase homology <TDS>	
P;180-462/Domain: thymidylate synthase homology <TDS>	
Query Match Score 46; DB 2; Length 462; Best Local Similarity 77.8%; Pred. No. 1.5; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy 82.1%;保守 Db 45 LIALPPCH 52	

**RESULT 38**  
**JCT7839**  
**uroplakin II protein - pig**  
**C Species: Sus scrofa domestica (domestic pig)**  
**C Date: 09-Dec-2002 #text\_change 09-Jul-2004**  
**C Accession: JC7839**  
**R; Kwon, D.N.; Seo, H.G.; Kim, J.H.**  
**Biochem. Biophys. Res. Commun. 233, 862-869, 2002**  
**A; Title: Cloning, sequencing, and expression analysis of the porcine uroplakin II gene.**  
**A; Reference number: JC7839; MUID:22050105; PMID:12054551**  
**A; Molecule type: DNA**  
**A; Cross-references: UNIPROT:Q95J04; UNIPARC:UPI000017CB44; GB:AY044180**  
**A; Residues: 1-184 <KWD>**  
**A; Cross-references: UNIPROT:Q95J04; UNIPARC:UPI000017CB44; GB:AY044180**  
**C; Comment: This protein with only one transmembrane domain, belongs to a group of integrins in both kidney and bladder.**  
**C; Genetics:**  
**A; Gene: uprI**  
**A; Introns: 26/1; 70/1; 116/2; 140/1**

Query Match Score 44; DB 2; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 1.4;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8  
 Db 45 LVALPPCH 52

**RESULT 39**  
**A49713**  
**uroplakin II precursor - bovine**  
**C; Species: Bos primigenius taurus (cattle)**  
**C; Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004**  
**C; Accession: A49713**  
**R; Lin, J.-H.; Wu, X.-R.; Kreibich, G.; Sun, T.T.**  
**J. Biol. Chem. 269, 1775-1784, 1994**  
**A; Title: Precursor sequence, processing, and urothelium-specific expression of a major 1**  
**A; Reference number: A49713; MUID:94124519; PMID:7507484**  
**A; Accession: A49713**  
**A; Status: preliminary**  
**A; Molecule type: mRNA**  
**A; Cross-references: <LINS>**  
**C; Keywords: glycoprotein; membrane bound; transmembrane protein**  
**C; Residues: 1-185 <LINS>**  
**A; Reference number: A49713; MUID:94124519; PMID:7507484**  
**A; Accession: A49713**  
**A; Status: preliminary**  
**A; Molecule type: mRNA**  
**A; Cross-references: <LINS>**  
**C; Keywords: glycoprotein; membrane bound; transmembrane protein**  
**C; Residues: 1-185 <LINS>**

Query Match Score 44; DB 2; Length 185;  
 Best Local Similarity 87.5%; Pred. No. 1.4;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8  
 Db 46 LVALPPCH 53

**RESULT 40**  
**YBYYT**  
**thymidylate synthase (EC 2.1.1.45) - yeast (Saccharomyces cerevisiae)**  
**N; Alternative names: protein O2950; protein YOR074C**  
**C; Species: Saccharomyces cerevisiae**  
**C; Date: 31-Mar-1993 #sequence\_revision 13-Mar-1997 #text\_change 05-Oct-2004**  
**C; Accession: S66957; A29546**  
**R; Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.**  
**Submitted to the Protein Sequence Database, July 1996**  
**A; Reference number: S66929**  
**A; Accession: S66957**  
**A; Molecule type: DNA**  
**A; Residues: 1-259 <BOH>**  
**A; Cross-references: UNIPROT:P06785; UNIPARC:UPI0000168414; EMBL:Z74982; NID:91420228; PI**  
**A; Experimental source: strain S288C**  
**R; Taylor, G.R.; Lagosky, P.A.; Storms, R.K.; Haynes, R.H.**  
**J. Biol. Chem. 262, 5298-5307, 1987**

PROC. Natl. Acad. Sci. U.S.A. 83, 3604-3608, 1986  
 A; Title: The A-T-rich genome of Herpesvirus saimiri contains a highly conserved gene for  
 A; Reference number: A26269; MUID:86233282; PMID:3012520  
 A; Accession: A26269  
 A; Molecule type: DNA  
 A; Residues: 1-294 <HON>  
 A; Cross-references: UNIPARC:UPI00001378D3; GB:MI3190; NID:9331074; PIDN:AAA46175.1;  
 C; Superfamily: thymidylate synthase; thymidylate synthase homology  
 C; Keywords: deoxyribonucleotide biosynthesis; methyltransferase  
 P; 11-294/Domain: thymidylate synthase homology <rD5>  
 P; 176/Active site: Cys #status predicted

Query Match Score 44; DB 1; Length 294;  
 Best Local Similarity 78.6%; Pred. No. 2.2;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 171 MALPPCHVL 179

Db 171 MALPPCH 177

RESULT 45  
 S73842 thymidylate synthase (EC 2.1.1.45) - Mycoplasma pneumoniae (strain ATCC 29342)  
 N; Alternative names: hypothetical protein F10\_orf328  
 A; Variety: ATCC 29342  
 C; Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
 C; Accession: S73842; S49072  
 R; Hummelrich, R.; Hilbert, H.; Plagens, H.; Pirtl, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A; Reference number: S73327; MUID:97105885; PMID:948633  
 A; Accession: S73842  
 A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-328 <HIM>  
 A; Cross-references: UNIPARC:UPI0000165596; EMBL:AE000050; SB:JU0089; NID:91674197; PIDN:  
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 R; Proft, T.; Herrmann, R.  
 Mol. Microbiol. 13, 337-348, 1994  
 A; Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae  
 A; Reference number: S49059; MUID:95075318; PMID:7984111  
 A; Accession: S49072  
 A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 204-244 'F' 252; 'LSYGH' 258 259 PRO>  
 A; Cross-references: UNIPARC:UPI000016F33F; EMBL:232654; NID:9474094; PIDN:CAA83575.1; PI  
 A; Experimental source: clone F10-2C  
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
 C; Genetics:  
 A; Gene: thyA  
 A; Genetic code: SGCG3  
 C; Superfamily: thymidylate synthase; thymidylate synthase homology  
 C; Keywords: deoxyribonucleotide biosynthesis; methyltransferase  
 P; 42-328/Domain: thymidylate synthase homology <rD5>

Query Match Score 44; DB 2; Length 328;  
 Best Local Similarity 77.8%; Pred. No. 2.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 206 MALPPCHSL 214

RESULT 46  
 T01684 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - maize  
 C; Species: Zea mays (maize)  
 C; Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 31-Dec-2004  
 C; Accession: T01684  
 R; Cox, K.M.; Robertson, D.; Rites, R.C.  
 J. Bacteriol. 171, 1372-1378, 1989  
 A; Description: Cloning of a cDNA encoding the bifunctional dihydrofolate reductase-thymidylate synthase. A; Reference number: Z14392  
 A; Accession: T01684  
 A; Status: translated from GB/EMBL/DDJB  
 A; Molecule type: mRNA  
 A; Residues: 1-521 <COX>  
 A; Cross-references: UNIPROT:081395; UNIPARC:UPI000012388A6; EMBL:AF073488; NID:93309065;  
 C; Genetics:  
 C; Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate synthase homology <rD5>

Query Match Score 44; DB 2; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCH 8

Qy	2 MALPPCH 8 	Qy	2 MALPPCHAL 10 
Db	398 MALPPCH 404	Db	141 MALPPCHAL 149
<b>RESULT 47</b>			
T37719	thymidylate synthase-like DNA metabolism protein - fission yeast (Schizosaccharomyces pombe)	B8981	thymidylate synthase (BC 2.1.1.45) [imported] - Buchnera sp. (strain APS)
C:Species: Schizosaccharomyces pombe	C:Species: Buchnera sp.	C:Species: Buchnera sp.	C:Species: Buchnera sp. (strain APS)
C:Date: 03-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004	C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004	C:Accession: B84981	C:Accession: B84981
C:Accession: T37719	C:Accession: B84981	R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.	R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R: Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Lyne, M.H.	Nature 407, 81-86, 2000	A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.	A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
submitted to the EMBL Data Library, August 1999	A:Reference number: A84930; PMID:10933077	A:Reference number: A84930; PMID:10933077	A:Reference number: A84930; PMID:10933077
A:Reference number: Z24739	A:Accession: B84981	A:Accession: B84981	A:Accession: B84981
A:Accession: T37719	A:Status: preliminary; translated from GB/EMBL/DBJ	A:Status: preliminary	A:Status: preliminary
A:Molecule type: DNA	A:Residues: 1-625 <STO>	A:Molecule type: DNA	A:Molecule type: DNA
A:Cross-references: UNIPROT:Q9UT77; UNIPARC:UPI00006C105; PIDN:CA852423.	A:Cross-references: UNIPARC:UPI00005E5A5; GB:AP000398; GSPDB:GN00144	A:Cross-references: UNIPARC:UPI00005E5A5; GB:AP000398; GSPDB:GN00144	A:Cross-references: UNIPARC:UPI00005E5A5; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain 972h-; cosmid c1551			
C:Genetics:	C:Genetics:	C:Genetics:	C:Genetics:
A:Gene: SPDB:SPAC15B1.04	A:Gene: thyA; BU440	C:Superfamily: thymidylate synthase; thymidylate synthase homology	C:Superfamily: thymidylate synthase; thymidylate synthase homology
A:Map position: 1	A:Map position: 1	C:Keywords: methyltransferase	C:Keywords: methyltransferase
Query Match	78.6%; Score 44; DB 2; Length 625;	Query Match	76.8%; Score 43; DB 2; Length 264;
Best Local Similarity	100.0%; Pred. No. 4.4; Mismatches 0; Gaps 0;	Best Local Similarity	77.8%; Pred. No. 2.9; Mismatches 0; Gaps 0;
Matches 7; Conservative	0; Indels 0; Gaps 0;	Matches 7; Conservative	0; Indels 0; Gaps 0;
Qy	2 MALPPCH 8 	Qy	2 MALPPCHAL 10 
Db	492 MALPPCH 498	Db	141 MALPPCHAL 149
<b>RESULT 48</b>			
G82569	thymidylate synthase Xf2332 [imported] - Xylella fastidiosa (strain 9a5c)	B80579	thymidylate synthase (ts) (tsase) [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Xylella fastidiosa	C:Species: Mycoplasma pulmonis	C:Species: Mycoplasma pulmonis	C:Species: Mycoplasma pulmonis
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004	C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004	C:Accession: B90579	C:Accession: B90579
C:Accession: G82569	R:Chambaud, I.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.	R:Chambaud, I.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.	R:Chambaud, I.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
R:Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen	Nature 406, 151-157, 2000	Nucleic Acids Res. 29, 2145-2153, 2001	Nucleic Acids Res. 29, 2145-2153, 2001
Nature 406, 151-157, 2000	A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.	A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmo	A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmo
A:Reference number: A82515; PMID:20365717; PMID:10910347	A:Reference number: A99328; PMID:12267165; PMID:11353084	A:Reference number: A99512; PMID:21267165; PMID:11353084	A:Reference number: A99512; PMID:21267165; PMID:11353084
A:Note: for a complete list of authors see reference number A99328 below	A:Note: for a complete list of authors see reference number A99328 below	A:Note: for a complete list of authors see reference number A99512; PMID:21267165; PMID:11353084	A:Note: for a complete list of authors see reference number A99512; PMID:21267165; PMID:11353084
A:Status: preliminary	A:Status: preliminary	A:Status: preliminary	A:Status: preliminary
A:Molecule type: DNA	A:Molecule type: DNA	A:Molecule type: DNA	A:Molecule type: DNA
A:Residues: 1-264 <SIM>	A:Residues: 1-286 <KUR>	A:Residues: 1-286 <KUR>	A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q9PB13; UNIPARC:UPI00001378F3; GB:AE004044; GB:AE003849; NID	A:Cross-references: UNIPARC:UPI00001378F2; GB:AL445566; PID:g14089953; PID:g14089953; PID:g14089953	A:Cross-references: UNIPARC:UPI00001378F2; GB:AL445566; PID:g14089953; PID:g14089953; PID:g14089953	A:Cross-references: UNIPARC:UPI00001378F2; GB:AL445566; PID:g14089953; PID:g14089953; PID:g14089953
A:Experimental source: strain 9a5c			
R:Simpson, P.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carrasco, D.M.; Carreiro, H.; as-Neto, R.; Docena, C.; Bl-Dorrry, H.; Faincani, A.P.; Ferreira, A.J.S.	R:Simpson, P.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.E.A.; Carrasco, D.M.; Carreiro, H.; as-Neto, R.; Docena, C.; Bl-Dorrry, H.; Faincani, A.P.; Ferreira, A.J.S.	R:Simpson, P.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.E.A.; Carrasco, D.M.; Carreiro, H.; as-Neto, R.; Docena, C.; Bl-Dorrry, H.; Faincani, A.P.; Ferreira, A.J.S.	R:Simpson, P.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.E.A.; Carrasco, D.M.; Carreiro, H.; as-Neto, R.; Docena, C.; Bl-Dorrry, H.; Faincani, A.P.; Ferreira, A.J.S.
A:Authors: Ferreira, V.C.A.; Petro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laing, A.; Marques, M.V.; Martins, E.C.; Marin, C.L.; Menck, C.F.M.; Miracca, E.C.; Miyaki, D.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.G.; Sawaak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tschakko, M.H.; Vallada, H.; Van Sluys, M.A.; Vesjovski-Almeida, S.; Vettore, A.L.; Vettore, A.L.	A:Authors: Ferreira, V.C.A.; Petro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laing, A.; Marques, M.V.; Martins, E.C.; Marin, C.L.; Menck, C.F.M.; Miracca, E.C.; Miyaki, D.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.G.; Sawaak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tschakko, M.H.; Vallada, H.; Van Sluys, M.A.; Vesjovski-Almeida, S.; Vettore, A.L.; Vettore, A.L.	A:Authors: Ferreira, V.C.A.; Petro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laing, A.; Marques, M.V.; Martins, E.C.; Marin, C.L.; Menck, C.F.M.; Miracca, E.C.; Miyaki, D.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.G.; Sawaak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tschakko, M.H.; Vallada, H.; Van Sluys, M.A.; Vesjovski-Almeida, S.; Vettore, A.L.; Vettore, A.L.	A:Authors: Ferreira, V.C.A.; Petro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laing, A.; Marques, M.V.; Martins, E.C.; Marin, C.L.; Menck, C.F.M.; Miracca, E.C.; Miyaki, D.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.G.; Sawaak, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tschakko, M.H.; Vallada, H.; Van Sluys, M.A.; Vesjovski-Almeida, S.; Vettore, A.L.; Vettore, A.L.
A:Content: annotation	A:Content: annotation	A:Content: annotation	A:Content: annotation
C:Genetics:	C:Genetics:	C:Genetics:	C:Genetics:
A:Gene: XF2332	C:Superfamily: thymidylate synthase; thymidylate synthase homology	C:Superfamily: thymidylate synthase; thymidylate synthase homology	C:Superfamily: thymidylate synthase; thymidylate synthase homology
Qy	76.8%; Score 43; DB 2; Length 264;	Qy	76.8%; Score 43; DB 2; Length 264;
Best Local Similarity	88.9%; Pred. No. 2.9; Mismatches 0; Gaps 0;	Best Local Similarity	88.9%; Pred. No. 2.9; Mismatches 0; Gaps 0;
Matches 8; Conservative	1; Indels 0; Gaps 0;	Matches 8; Conservative	1; Indels 0; Gaps 0;
Search completed: February 17, 2006, 02:44:29			
Job time : 59 secs			

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Gencore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: February 17, 2006, 02:36:31 ; Search time 227 Seconds

(31.081 Million cell updates/sec  
 31.081 Million cell updates/secScoring table: BLOSSM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs., 705528306 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summariesDatabase : UniProt 05-80.\*\*  
 1: uniprot\_sprot:/\*  
 2: uniprot\_trembl:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

\* Query Score No. Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	222	2	Q8CZH6_MOUSE	Q8CZH6 mus musculu
2	56	100.0	222	2	Q8CZR3_MOUSE	Q8CZR3 mus musculu
3	56	100.0	230	2	Q8WTK4_HUMAN	Q8WTK4 homo sapien
4	56	100.0	279	2	Q8YK3_HUMAN	Q8YK3 Homo sapien
5	56	100.0	56	307	1	TYSY_MOUSE
6	56	100.0	56	307	1	TYSY_RAT
7	56	100.0	307	2	Q54AL2_MOUSE	
8	56	100.0	307	2	Q8UDV6_MOUSE	
9	56	100.0	307	2	Q9DDH1_MOUSE	
10	56	100.0	312	1	TYSY_HUMAN	
11	56	100.0	313	2	Q53BE7_HUMAN	
12	56	100.0	313	2	Q53J97_HUMAN	
13	56	100.0	318	2	Q6P045_BRARE	
14	56	100.0	319	2	Q7ZU17_BRARE	
15	56	100.0	307	2	Q9DGH5_BRARE	
16	52	92.9	264	1	TYSY_AZORE	
17	52	92.9	264	1	TYSY_NEIMB	
18	52	92.9	264	1	TYSY_NEIMB	
19	52	92.9	264	1	TYSY_PSEAB	
20	52	92.9	264	2	Q5P732_NEIG1	
21	52	92.9	265	1	TYSY_NEIGO	
22	52	92.9	266	1	TYSY_BIFLO	
23	52	92.9	316	2	Q91CH7_RALPH	
24	51	91.1	295	2	Q9BZ02_RALPH	
25	51	91.1	337	1	TYSY_HHV8	
26	51	87.5	264	1	TYSY_CHRVO	
27	49	87.5	314	1	TYSY_LISTIN	
28	49	87.5	314	1	TYSY_LISTINF	
29	49	87.5	314	1	TYSY_LISNO	
30	48	85.7	63	2	Q7t4R2_9GAMA	
31	48	85.7	124	2	Q8QYZ3_RTRV	

1	TYSY-EHV2	equine	herp	Q60382	methylcocc
289	1	TYSY-AGABI	agricus	Q62288	baronella
106	47	83.9	OP947	Q6ffz91	bordetella
107	47	83.9	J223	Q6ffz13	bordetella
108	47	83.9	TYSY-BORR	Q7w1a9	bordetella
109	47	83.9	TYSY-BORR	Q7vye3	bordetella
110	47	83.9	TYSY-PSEBM	Q8bcn3	bordetella
111	47	83.9	TYSY-PSEBM	Q87ul4	pseudomonas
112	47	83.9	Q4ZLUV5	Q4zlv5	pseudomonas
113	47	83.9	PESY	Q4K480	pseudomonas
114	47	83.9	Q9Rb67	Q9r67	deinococcus
115	47	83.9	DIRA	Q95mt2	trypanosoma
116	47	83.9	TYCR	Q95ny4	trypanosoma
117	47	83.9	TYCR	Q963s7	trypanosoma
118	47	83.9	TYCR	Q963s8	trypanosoma
119	47	83.9	TYCR	Q95ni3	trypanosoma
120	47	83.9	TYCR	Q95ns0	trypanosoma
121	47	83.9	TYCR	Q95nx3	trypanosoma
122	47	83.9	TYCR	Q95x22	plasmid
123	47	83.9	PLACH	P16126	leishmania
124	47	83.9	PLACH	P07382	leishmania
125	47	83.9	PLACH	Q8M0V1	LEICH
126	47	83.9	PLACH	Q8M0V3	LEICH
127	47	83.9	PLACH	Q8Mxb7	leishmania
128	47	83.9	PLACH	Q8Mzb8	leishmania
129	47	83.9	PLACH	Q4qiz1	leishmania
130	47	83.9	PLACH	Q27793	trypanosoma
131	47	83.9	PLACH	Q8t5t8	trypanosoma
132	47	83.9	PLACH	Q8t5t9	trypanosoma
133	47	83.9	PLACH	Q4n262	theileria
134	47	83.9	PLACH	Q4u9g5	theileria
141	47	83.9	PLACH	P20712	plasmidium
136	47	83.9	PLACH	Q4ywh2	plasmidium
137	47	83.9	PLACH	Q2713	plasmidium
138	47	83.9	PLACH	Q7rgh7	plasmidium
139	47	83.9	PLACH	Q95us9	plasmidium
140	47	83.9	PLACH	P13922	plasmidium
141	47	83.9	PLACH	Q8i1r6	plasmidium
142	47	83.9	PLACH	Q07422	toxoplasma
143	47	83.9	PLACH	Q02604	plasmidium
144	46	82.1	PLACH	Q9z1G0	enterococcus
145	46	82.1	PLACH	Q9wb13	iride
146	46	82.1	PLACH	Q9wb13	iride
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159	46	82.1	PLACH	Q9wb13	iride
160	45	80.4	PLACH	Q67048	staphylococ
161	45	80.4	PLACH	P604m4	staphylococ
162	45	80.4	PLACH	P61047	staphylococ
163	45	80.4	PLACH	Q5mp6	staphylococ
164	44	78.6	PLACH	Q7bwg2	staphylococ
165	44	78.6	PLACH	Q7d159	staphylococ
166	44	78.6	PLACH	Q4L6D7	staphylococ
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168	44	78.6	PLACH	Q6Wb0	harmannell
169	44	78.6	PLACH	Q8mv96	mastigamoeb
170	44	78.6	PLACH	Q9ue88	homo sapien
171	44	78.6	PLACH	Q9BMD8	babesia bovis
172	44	78.6	PLACH	Q9tu13	cryptococcus
173	44	78.6	PLACH	Q6X183	bacteriophaga
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300	44	78.6	PLACH	Q6ffz91	bacteriophaga

251	42	75.0	312	2	Q9N588 CABEL	Q99588 caenorhabdi	Q6kgf1 bacteriophaga
252	42	75.0	315	2	Q607X6 CABBR	Q9y052 caenorhabdi	Q9i10r9 pseudomonas
253	42	75.0	315	2	Q9Y052 CABBR	Q9y052 caenorhabdi	Q9vms0 oryza sativ
254	42	75.0	389	2	Q611Z9 CABER	Q611z9 caenorhabdi	Q7qhc2 anopheles g
255	42	75.0	780	2	Q4QAU0 LEIMA	Q9au0 leishmania	Q7ixub plasmoidium
256	41	73.2	287	1	TYSY MYCSE	P7t469 mycoplasma	Q7tex6 brucella ab
257	41	73.2	318	1	TYSY LACIC	Q5Ktl6 lactobacill	P0a4d9 brucella me
258	41	73.2	584	2	Q4SP52 TETING	Q5Kbd6 bacillus cl	P0a4eo brucella su
259	40.5	72.3	513	2	Q5TBD6 HUMAN	Q5bp22 tetradon n	Q5i129 magnaporthe
260	40.5	72.3	551	1	KIF12 HUMAN	Q5bbd6 homo sapien	Q43476 hordeum vul
261	40.5	72.3	646	2	Q5TB0 HUMAN	Q5b60 homo sapien	Q7xec2 oryza sativ
262	40	71.4	168	1	Q69RP0 ORYSA	Q6rp0 oryza sativ	Q7pxw6 ustilago ma
263	40	71.4	264	1	TYSY BACID	Q7n8u4 photorhabdu	Q9w081 drosophila
264	40	71.4	264	1	TYSY BACKS	Q5db1 bacillus cl	Q7xec7 oryza sativ
265	40	71.4	264	1	TYSY SALPA	Q5p66 salmonella	Q5i102 magnaporthe
271	40	71.4	264	1	TYSY SALTI	Q8412 escherichia	Qmvr4 bacillus ce
266	40	71.4	264	1	TYSY ECOL6	Q8a885 escherichia	Q8id95 plasmid
273	40	71.4	264	1	TYSY ECOLI	Q8a884 escherichia	Q84qa4 oryza sativ
274	40	71.4	264	1	TYSY SHFL	Q8a886 erwinia car	Q7xec2 oryza sativ
275	40	71.4	264	1	TYSY PHOU	Q8pd46 xanthomonas	Q7rqk2 plasmid
276	40	71.4	264	1	TYSY XANGP	Q8pc7 xanthomonas	Q9yt55 plasmid
277	40	71.4	264	1	TYSY XANOR	Q9wb5 xanthomonas	Q583w8 trypanosoma
278	40	71.4	264	1	TYSY SALTY	Q8zma9 salmonella	Qmvr4 bacillus ce
279	40	71.4	264	1	TYSY SHEON	Q8ph91 shewanella	Q6zpb5 homo sapien
280	40	71.4	264	1	TYSY YERPS	F48464 shigella fi	Q88ij2 pseudomonas
281	40	71.4	264	1	TYSY XANC	Q8pd46 xanthomonas	Q7rqk2 plasmid
282	40	71.4	264	1	TYSY XANGP	Q8pc7 xanthomonas	Q9w4g5 drosophila
283	40	71.4	264	1	TYSY XANOR	Q9wb5 xanthomonas	Q7xec7 oryza sativ
284	40	71.4	264	1	TYSY XENNE	Q8re8 xenorhabdus	Q651ko oryza sativ
285	40	71.4	264	1	TYSY YERPS	Q8ah91 yersinia pe	Q45953 canenorhabdi
286	40	71.4	264	1	TYSY YERPS	Q67f79 yersinia ps	Q5nae2 oryza sativ
287	40	71.4	264	2	Q57KB6 SALCH	Q57kb6 salmonella	Q92m31 rhizobium m
288	40	71.4	264	2	Q8GMW7 ECOLI	Q8gmw7 escherichia	Q8k9c3 buchnera ap
289	40	71.4	264	2	Q4UR35 XANCP	Qur35 xanthomonas	Q7ypg6 rhizostoma
290	40	71.4	266	1	TYSY NOCPA	Q57m1 sym	Q5wqo cryptobacte
291	40	71.4	368	2	TYSY LETIX	Q58p17 noardiida fa	Q98gx3 rhizobium
292	40	71.4	673	2	TYSY MESPIL	Q6f510 leifsonia x	Q59kj7 cryptococci
293	39	69.6	69	2	Q6WTC0 BKRV4	Q6145 mesoplasma	Q520p2 magnaporthe
294	39	69.6	69	2	Q9ND3 TRISP	Q6wico bacteriophora	Q7pvk0 ANOGA
295	39	69.6	76	2	Q4NNDD3 TRICHL	Q9ndd3 trichinella	Q52t8 CHICK
296	39	69.6	106	2	Q4IN25 GBZE	Q1inz5 gibberella	P25283 haemophilus
297	39	69.6	146	2	Q5PTX45 ANOGR	Q5trx45 anophelis g	Q4rd12 tetrodon n
298	39	69.6	196	2	Q7S072 NEUCR	Q7s072 neurospora	Q5wqo tetrodon n
299	39	69.6	213	2	Q6FVG7 CINGA	Q48t08 tetrodon n	Q59kj7 oryza sativ
300	39	69.6	264	1	Q5FN18 GIJOX	Q69uk3 oryza sativ	Q520p2 magnaporthe
301	39	69.6	281	1	TYSY GEOTRM	Q55ni8 gluconobact	Q6inw3 xenopus lae
302	39	69.6	286	2	Q4SS16 TETING	Q583u6 tetrodon n	Q572t8 mimivirus
303	39	69.6	331	2	Q5PTX45 ANOGR	Q8ch55 mus musculu	Q57328 gallus gall
304	39	69.6	336	2	Q6FVG7 CINGA	Q65fxg7 candida gla	Q66ih1 xenopus tro
305	39	69.6	371	2	Q5LSJ8 SLIPPO	Q518j8 silicibacte	Q8ziw4 yersinia pe
311	38	67.9	396	2	Q6P625 XENTR	Q6wt25 nanophtycet	Q08463 rattus norv
312	38	67.9	475	2	Q6N733 RHOPIA	Q56733 rhodospseud	Q794z1 oryza sativ
307	39	69.6	693	2	Q8CD05 MOUSE	Q6cd05 geobacillus	Q53qt2 mus musculu
313	38	67.9	142	2	Q4SL59 TETING	Q8b159 tetrodon n	Q549t8 homo sapien
314	38	67.9	142	2	Q4TX10 AZOVI	Q678j8 lymphocysti	Q502y3 homo sapien
309	38	67.9	122	1	RNPA SYNP6	Q18839 caenorhabdi	Q58563 rubella vir
310	38	67.9	131	2	Q9C0N2 MOUSE	Q93408 salmella	Q21480 rubella vir
305	39	69.6	396	2	Q6P625 XENTR	Q6p625 xenopus tro	Q5vata1 drosophila
311	38	67.9	142	2	TAKL1 MOUSE	Q6n733 rhoopseud	Q9xeg1 grosserypum h
312	38	67.9	233	2	Q8TC19 HUMAN	Q6t255 rhodospseud	P243036 dictyosteli
313	38	67.9	142	2	Q6DFP7 RAT	Q6dfp7 rattus norv	Q8t202 hom sapien
308	38	67.9	111	2	Q678j8 917R	Q6ix1 azotobacter	Q8t228 dictyosteli
315	38	67.9	143	2	Q18839 CABEL	Q544c0 mus musculu	Q9ctg5 mouse
316	38	67.9	231	2	Q93408 SALTI	Q7xyy9 griffithsia	Q7tnnn1 mouse
317	38	67.9	233	2	Q53V5 THBT8	Q53ys5 thermus the	Q93x70 sorghum bic
318	38	67.9	233	2	QBY9A1 LISSMO	Q92e227 listeria mo	Q88fl4 pseudomonas
319	38	67.9	233	2	Q72B285 LISSMP	Q72B285 listeria mo	Q9ctg5 mouse
320	38	67.9	242	1	TAKL1 HUMAN	Q57077 homo sapien	Q7tnnn1 mouse
321	38	67.9	264	1	TYSY BUCBP	P59427 buchnera ap	Q93x70 sorghum bic
322	38	67.9	264	1	TYSY PORGT	Q7mtb5 porphyromon	Q88fl4 pseudomonas
323	38	67.9	292	2	Q9YVKA MSBPV	Q9yvka melanoplus	Q88fl4 pseudomonas

				P09933	sus scrofa
397	35	62.5	Q6BL85	DEBBA	926
	147	2	Q9YHE9	CYPICA	926.5
	35	62.5	Q96DN7	HUMAN	926.5
	398	2	Q4LKA1	BURK	926.5
	35	62.5	Q4NNG2	9DBLT	926.5
	157	2	Q7QD90	CHICK	926.5
	400	35	Q9UTD1	SCHPO	926.5
	401	35	Q6TII03	DROME	926.5
	402	35	Q5JLS3	ORYZA	926.5
	403	35	Q5MHD2	9SPHN	926.5
	404	35	CRF PIG		926.5
	411	35	Q9ATW6	HUMAN	926.5
	412	35	Q5NTA6	ORYZA	926.5
	413	35	Q5V39	HUMAN	926.5
	414	35	Q7D71	DESVDH	926.5
	415	35	Q6WT51	9TREM	926.5
	416	35	Q8TB95	METKA	926.5
	417	35	Q5J126	SYNPW	926.5
	418	35	Q5UJ26	ORYZA	926.5
	419	35	Q4RKZ7	TESTING	926.5
	420	35	Q6NQ99	CORDI	926.5
	421	35	Q7SY5	NITPUD	926.5
	422	35	Q56B5	9CRAUD	926.5
	423	35	Q7W9G9	BORPA	926.5
	424	35	Q7WH93	BORBR	926.5
	425	35	Q7W9E3	PROMM	926.5
	426	35	Q7UNIO	RHOBA	926.5
	427	35	Q7XK84	BACHID	926.5
	428	35	Q63551	BURK	926.5
	429	35	Q6M70	BURMA	926.5
	430	35	Q9UHQ5	HALIVO	926.5
	431	35	Q7XOQ5	HUMAN	926.5
	432	35	Q6AKA2	HUMAN	926.5
	433	35	Q4LM44	9BURK	926.5
	434	35	Q7MDU	RICPR	926.5
	435	35	TRMD	RICRY	926.5
	436	35	Q7PV6	FUSNN	926.5
	437	35	Q8REZ7	FUSNN	926.5
	438	35	Q7XEB6	ORYSA	926.5
	439	35	Q5D975	SCEJJA	926.5
	440	35	Q6LGY1	CLEBR	926.5
	441	35	Q51WF2	MAGGR	926.5
	442	35	Q7XKA0	ORYSA	926.5
	443	35	Q4TS23	9SPHN	926.5
	444	35	KARCI	CABEL	926.5
	445	35	Q5LHA5	BACFN	926.5
	446	35	Q6AWB5	BACFR	926.5
	452	35	Q5NIV8	SNTNP6	926.5
	453	35	DRTS	CRFTA	926.5
	454	35	Q60523	CLEBR	926.5
	449	35	Q20584	CBEL	926.5
	455	35	Q75KL2	ORYSA	926.5
	456	35	Q6Q156	9BLT	926.5
	457	35	Q8S1B2	ORYSA	926.5
	458	35	Q9V7E0	DROME	926.5
	459	35	Q4NNK1	9DBLT	926.5
	460	35	Q8SSY2	ORYSA	926.5
	461	35	Q8MLAB8	DROME	926.5
	462	35	Q7FAB5	ORYSA	926.5
	463	35	FULL YEAST		926.5
	464	35	Q6D065	BRWCT	926.5
	465	35	Y304	ERWC	926.5
	466	35	Q8LN79	ORYSA	926.5
	467	35	Q6DB09	XENLA	926.5
	468	35	Q8MLAG9	DROME	926.5
	469	35	Q5T05	TESTING	926.5
	470	35	Q9YHE9	CYPICA	926.5
	471	35	Q9Wq6	aspergillus	926.5
	472	35	Q7PQX6	anophelis	926.5
	473	35	Q9B7J5	drosophila	926.5
	474	35	Q97867	DROME	926.5
	475	35	Q4Fy5	leishmania	926.5
	476	35	Q8IBP7	agrobacteri	926.5
	477	35	Q6BD67	arthrobacte	926.5
	478	35	Q4smt5	tetradodon	926.5
	479	35	Q9W437	DROME	926.5
	480	35	Q804W6	FUGR	926.5
	481	35	Q9qvt6	rattus	926.5
	482	35	Q9qnd0	mus musculu	926.5
	483	35	Q4t37	leishmania	926.5
	484	35	Q80hs3	ORYHO1	926.5
	485	35	Q9k17	homo sapien	926.5
	486	35	Q82DD3	streptomyce	926.5
	487	35	Q4x3e8	plasmoidium	926.5
	488	35	Q99nd0	mus musculu	926.5
	489	35	Q4t37	metanopyru	926.5
	490	34	Q80799	mus musculu	926.5
	491	34	Q9k17	leishmania	926.5
	492	34	Q81ES2	PLACH	926.5
	493	34	Q4t37	hepatitis e	926.5
	494	34	Q4t37	hepatitis e	926.5
	495	34	Q88gzt	pseudomonas	926.5
	496	34	Q8BGZ7	PSEPK	926.5
	497	34	Q617ZK4	ORYSA	926.5
	498	34	Q9d47	archaeoglob	926.5
	499	34	Q4j7v3	sulfolobus	926.5
	500	34	Q8Bn63	mus musculu	926.5
	501	34	Q519v8	sorghum bic	926.5
	502	34	Q9mu0	homo sapien	926.5
	503	34	Q8w34	homo sapien	926.5
	504	34	Q9da7	mus musculu	926.5
	505	34	Q5jy54	homo sapien	926.5
	506	34	Q97A1	pseuds	926.5
	507	34	Q75QP2	RANCA	926.5
	508	34	Q9mu0	HUMAN	926.5
	509	34	Q8C3A5	mus musculu	926.5
	510	34	Q9y78	LAMFL	926.5
	511	34	Q56X15	XANTHOMONAS	926.5
	512	34	Q7w364	bordetella	926.5
	513	34	Q7we12	BORBR	926.5
	514	34	Q812E6	BORPE	926.5
	515	34	Q6s8Q9	ORYSA	926.5
	516	34	Q6ZRW3	HUMAN	926.5
	517	34	Q95mi6	bos taurinus	926.5
	518	34	P01142	ovis aries	926.5
	519	34	Q82947	oryza sativ	926.5
	520	34	Q6zu23	homo sapien	926.5
	521	34	Qd77y	vibrio vuln	926.5
	522	34	Q7me8	vibrio vuln	926.5
	523	34	Q6j9lo	gorilla gorilla	926.5
	524	34	Q75h84	oryza sativ	926.5
	525	34	Q41250	azotobacter	926.5
	526	34	Q6lsaa7	photobacter	926.5
	527	34	Q4wn04	ASPERGILLUS	926.5
	528	34	Q4ltv9	burkholderi	926.5
	529	34	Q4t37	tetradodon	926.5
	530	34	Q82z63	ratsonia s	926.5
	531	34	Q926c4	rhizobium m	926.5
	532	34	Q6zmld1	homo sapien	926.5
	533	34	Q8hvj6	boltenii vi	926.5
	534	34	Q60a17	methylococc	926.5
	535	34	Q50n14	ENTHIA	926.5
	536	34	Q9i9n5	brachydano	926.5
	537	34	Q03070	rattus norv	926.5
	538	34	Q63xq0	burkholderi	926.5
	539	34	Q624q1	caterozabdi	926.5
	540	34	Q6oxd1	mus musculu	926.5
	541	34	Q6au5	oryza sativ	926.5
	542	34	Q6gn5	xenopus lae	926.5
	543	34	Q6qnt5	debatomyce	926.5
	544	34	Q8mlag9	drosophila	926.5
	545	34	Q5t05	TESTING	926.5
	546	34	Q9YHE9	CYPICA	926.5
	547	34	Q9qvt6	rattus	926.5
	548	34	Q9qnd0	mus musculu	926.5
	549	34	Q4t37	metanopyru	926.5
	550	34	Q80799	mus musculu	926.5
	551	34	Q4t37	leishmania	926.5
	552	34	Q81ES2	PLACH	926.5
	553	34	Q9k17	metanopyru	926.5
	554	34	Q9qvt6	rattus	926.5
	555	34	Q9qnd0	mus musculu	926.5
	556	34	Q4t37	hepatitis e	926.5
	557	34	Q80799	mus musculu	926.5
	558	34	Q4t37	hepatitis e	926.5
	559	34	Q9qvt6	metanopyru	926.5
	560	34	Q9qnd0	mus musculu	926.5
	561	34	Q4t37	hepatitis e	926.5
	562	34	Q80799	mus musculu	926.5
	563	34	Q4t37	hepatitis e	926.5
	564	34	Q80799	mus musculu	926.5
	565	34	Q4t37	hepatitis e	926.5
	566	34	Q80799	mus musculu	926.5
	567	34	Q4t37	hepatitis e	926.5
	568	34	Q80799	mus musculu	926.5
	569	34	Q4t37	hepatitis e	926.5
	570	34	Q80799	mus musculu	926.5
	571	34	Q4t37	hepatitis e	926.5
	572	34	Q80799	mus musculu	926.5
	573	34	Q4t37	hepatitis e	926.5
	574	34	Q80799	mus musculu	926.5
	575	34	Q4t37	hepatitis e	926.5
	576	34	Q80799	mus musculu	926.5
	577	34	Q4t37	hepatitis e	926.5
	578	34	Q80799	mus musculu	926.5
	579	34	Q4t37	hepatitis e	926.5
	580	34	Q80799	mus musculu	926.5
	581	34	Q4t37	hepatitis e	926.5
	582	34	Q80799	mus musculu	926.5
	583	34	Q4t37	hepatitis e	926.5
	584	34	Q80799	mus musculu	926.5
	585	34	Q4t37	hepatitis e	926.5
	586	34	Q80799	mus musculu	926.5
	587	34	Q4t37	hepatitis e	926.5
	588	34	Q80799	mus musculu	926.5
	589	34	Q4t37	hepatitis e	926.5
	590	34	Q80799	mus musculu	926.5
	591	34	Q4t37	hepatitis e	926.5
	592	34	Q80799	mus musculu	926.5
	593	34	Q4t37	hepatitis e	926.5
	594	34	Q80799	mus musculu	926.5
	595	34	Q4t37	hepatitis e	926.5
	596	34	Q80799	mus musculu	926.5
	597	34	Q4t37	hepatitis e	926.5
	598	34	Q80799	mus musculu	926.5
	599	34	Q4t37	hepatitis e	926.5
	600	34	Q80799	mus musculu	926.5
	601	34	Q4t37	hepatitis e	926.5
	602	34	Q80799	mus musculu	926.5
	603	34	Q4t37	hepatitis e	926.5
	604	34	Q80799	mus musculu	926.5
	605	34	Q4t37	hepatitis e	926.5
	606	34	Q80799	mus musculu	926.5
	607	34	Q4t37	hepatitis e	926.5
	608	34	Q80799	mus musculu	926.5
	609	34	Q4t37	hepatitis e	926.5
	610	34	Q80799	mus musculu	926.5
	611	34	Q4t37	hepatitis e	926.5
	612	34	Q80799	mus musculu	926.5
	613	34	Q4t37	hepatitis e	926.5
	614	34	Q80799	mus musculu	926.5
	615	34	Q4t37	hepatitis e	926.5
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	622	34	Q80799	mus musculu	926.5
	623	34	Q4t37	hepatitis e	926.5
	624	34	Q80799	mus musculu	926.5
	625	34	Q4t37	hepatitis e	926.5
	626	34	Q80799	mus musculu	926.5
	627	34	Q4t37	hepatitis e	926.5
	628	34	Q80799	mus musculu	926.5
	629	34	Q4t37	hepatitis e	926.5
	630	34	Q80799	mus musculu	926.5
	631	34	Q4t37	hepatitis e	926.5
	632	34	Q80799	mus musculu	926.5
	633	34	Q4t37	hepatitis e	926.5
	634	34	Q80799	mus musculu	926.5
	635	34	Q4t37	hepatitis e	926.5
	636	34	Q80799	mus musculu	926.5
	637	34	Q4t37	hepatitis e	926.5
	638	34	Q80799	mus musculu	926.5</td

543	34	60.7	345	2	Q4YU44_PLABE	04yu44 plasmoidium	Q4qif0_leishmania	Q4qif0 LEIMA	930	2
544	34	60.7	348	2	Q7RFH4_PLABE	07rfh4 plasmoidium	Q8t3z2_tetradon n	936	2	
545	34	60.7	349	2	Q7RFH4_PLAYO	07rfh4 plasmoidium	Q8t3t3 toxoplasma	60.7	34	
546	34	60.7	349	2	Q63611_BALICA	063611 balanggloss	Q5kqu1 macaca fasc	60.7	34	
547	34	60.7	352	2	Q848M1_ORYSA	0848m1 oryza sativ	P33200 saccharomyc	969	2	
548	34	60.7	352	2	Q50170_MYCLE	050170 mycobacteri	PDR3_YEAST	969	2	
549	34	60.7	368	2	Q9CBB8_MYCLE	09ccb8 mycobacteri	Q6B1F6 YEAST	976	1	
550	34	60.7	377	2	Q51RP6_MAGRGR	09ccb6 magnaporthe	Q5B566 aspergillus	998	2	
551	34	60.7	382	2	Q6EN39_ORYSA	06en39 oryza sativ	Q5kqu2 macaca fasc	998	2	
552	34	60.7	385	2	Q7R786_PLAICH	07r786 plasmoidium	Q5kqu3 macaca fasc	1042	2	
553	34	60.7	398	2	Q7NAV2_BRORPA	07nav2 bordetella	Q5kqu3 MACFA ..	1042	2	
560	34	60.7	404	2	Q75BL2_ASHGO	075bl2 ashbya goss	Q5kqu4 ..	1042	2	
561	34	60.7	411	2	Q9ENU6_HUMAN	09enu6 homo sapien	Q5kqu5 ..	1042	2	
555	34	60.7	429	2	Q5AT07_ORYSA	05at07 oryza sativ	Q5kqu6 ..	1042	2	
556	34	60.7	443	2	Q69T50_ORYSA	069t50 oryza sativ	Q5kqu7 ..	1042	2	
557	34	60.7	443	2	Q84T99_ORYSA	084t99 oryza sativ	Q5kqu8 ..	1042	2	
558	34	60.7	450	2	Q4XVB7_PLAICH	04xvb7 plasmoidium	Q5kqu9 ..	1042	2	
559	34	60.7	459	2	Q4SDD9_TETING	04sdd9 tetraodion n	Q5kqu9 ..	1042	2	
566	34	60.7	480	2	Q7W92_CIRVO	07w92 chronobacte	Q5kqu9 ..	1042	2	
567	34	60.7	482	1	PAPE53_MOUSE	0ape53 mouse	Q5kqu9 ..	1042	2	
568	34	60.7	489	2	Q6QPZ2_9IACT	06qpz2 lactococcus	Q5kqu9 ..	1042	2	
562	34	60.7	467	2	Q5VR75_ORYSA	05vr75 oryza sativ	Q5kqu9 ..	1042	2	
563	34	60.7	467	2	Q84T99_ORYSA	084t99 oryza sativ	Q5kqu9 ..	1042	2	
564	34	60.7	468	1	CHIO_HUMAN	p52757 homo sapien	Q5kqu9 ..	1042	2	
565	34	60.7	474	2	Q41QJ4_GIBBERELLA	041qj4 gibberella	Q5kqu9 ..	1042	2	
566	34	60.7	480	2	Q7NW92_CHROMOBA	07nw92 chromobacte	Q5kqu9 ..	1042	2	
567	34	60.7	482	1	PAPE53_MOUSE	0ape53 mouse	Q5kqu9 ..	1042	2	
568	34	60.7	489	2	Q52RH3_MAGRGR	052rh3 magnaporthe	Q5kqu9 ..	1042	2	
569	34	60.7	508	2	Q4XV11_ASPPU	04xv11 aspergillus	Q5kqu9 ..	1042	2	
570	34	60.7	518	1	TH14_SICHO	p40386 s probable	Q5kqu9 ..	1042	2	
571	34	60.7	520	2	Q7X714_ORYSA	07x714 oryza sativ	Q5kqu9 ..	1042	2	
572	34	60.7	523	2	Q4Q336_LIshima	04q336 leishmania	Q5kqu9 ..	1042	2	
573	34	60.7	535	2	Q5TRM1_HUMAN	05trm1 homo sapien	Q5kqu9 ..	1042	2	
574	34	60.7	538	2	Q55V41_CRYNE	055v41 cryptococcu	Q5kqu9 ..	1042	2	
575	34	60.7	538	2	Q5KL40_CRYNE	05kl40 cryptococcu	Q5kqu9 ..	1042	2	
576	34	60.7	547	2	Q6R18_HUMAN	06r18 homo sapien	Q5kqu9 ..	1042	2	
577	34	60.7	548	2	Q8AVJ9_XENLIA	08avj9 xenopus lae	Q5kqu9 ..	1042	2	
578	34	60.7	548	2	Q5BL72_XENTR	05bl72 xenopus tro	Q5kqu9 ..	1042	2	
579	34	60.7	549	1	FZD7_XENIA	fzd7 xenia	Q5kqu9 ..	1042	2	
580	34	60.7	553	2	Q4T738_TETING	04t738 tetraodion n	Q5kqu9 ..	1042	2	
581	34	60.7	559	2	Q90T32_BRARE	090t32 brachydanio	Q5kqu9 ..	1042	2	
582	34	60.7	559	2	Q98512_BRARE	098512 brachydanio	Q5kqu9 ..	1042	2	
583	34	60.7	559	2	Q6NV44_BRARE	06nv44 brachydanio	Q5kqu9 ..	1042	2	
584	34	60.7	559	2	Q7S9R7_BRARE	07s9r7 brachydanio	Q5kqu9 ..	1042	2	
585	34	60.7	567	1	FZD7_CHICK	fzd7 chick	Q5kqu9 ..	1042	2	
586	34	60.7	572	1	PZD7_MOUSE	pzd7 mouse	Q5kqu9 ..	1042	2	
587	34	60.7	572	1	Q6Pb51_MOUSE	q6pb51 mus musculu	Q5kqu9 ..	1042	2	
588	34	60.7	574	1	FZDT_HUMAN	075084 aspergillus	Q5kqu9 ..	1042	2	
589	34	60.7	574	2	Q535F9_HUMAN	0535f9 homo sapien	Q5kqu9 ..	1042	2	
590	34	60.7	583	2	Q4Q9T0_LIHEMA	04q9t0 leishmania	Q5kqu9 ..	1042	2	
591	34	60.7	588	1	HDA10_RAT	0569c4 rattus norv	Q5kqu9 ..	1042	2	
592	34	60.7	600	2	Q6PBM7_BRARE	06pbm7 brachydanio	Q5kqu9 ..	1042	2	
593	34	60.7	603	2	Q4NTD7_9IBLT	04ntd7 anaeromykob	Q5kqu9 ..	1042	2	
594	34	60.7	603	2	Q4NTD7_9IBLT	04ntd7 anaeromykob	Q5kqu9 ..	1042	2	
595	34	60.7	626	2	Q4YU44_PLABE	04yu44 plasmoidium	Q5kqu9 ..	1042	2	
596	34	60.7	636	1	LRFN4_KOUSE	0535f9 mus musculu	Q5kqu9 ..	1042	2	
597	34	60.7	650	2	Q8C1J9_MOUSE	08c1j9 mus musculu	Q5kqu9 ..	1042	2	
598	34	60.7	666	1	HDA10_MOUSE	09h10 mouse	Q5kqu9 ..	1042	2	
599	34	60.7	683	2	Q9VH19_DROME	09vh19 drosophila	Q5kqu9 ..	1042	2	
600	34	60.7	727	2	Q4WRL9_ASPPU	04wrl9 aspergillus	Q5kqu9 ..	1042	2	
601	34	60.7	733	2	Q8YCW2_BRUME	08ycw2 brucella me	Q5kqu9 ..	1042	2	
602	34	60.7	740	2	Q5JUV6_HUMAN	05juv6 homo sapien	Q5kqu9 ..	1042	2	
603	34	60.7	750	2	Q810L8_MOUSE	0810l8 mouse	Q5kqu9 ..	1042	2	
604	34	60.7	764	2	Q9HP8_HUMAN	09hp8 homo sapien	Q5kqu9 ..	1042	2	
605	34	60.7	776	2	Q4IBX2_GIBZE	04ibx2 gibberella	Q5kqu9 ..	1042	2	
606	34	60.7	778	1	NTRK1_CHICK	0910n9 gallus gall	Q5kqu9 ..	1042	2	
607	34	60.7	829	1	KSR2_HUMAN	052ab6 homo sapien	Q5kqu9 ..	1042	2	
608	34	60.7	835	2	Q52B70_MAGRGR	052b70 magnaporthe	Q5kqu9 ..	1042	2	
609	34	60.7	841	2	Q94HS2_ORYSA	094hs2 oryza sativ	Q5kqu9 ..	1042	2	
610	34	60.7	842	2	Q7XGUB8_ORYSA	07xgub8 oryza sativ	Q5kqu9 ..	1042	2	
611	34	60.7	842	2	Q5AEU0_CANAL	05aeu0 canal	Q5kqu9 ..	1042	2	
612	34	60.7	891	2	Q8GHT8_PEBRE	08ght8 pseudomonas	Q5kqu9 ..	1042	2	
613	34	60.7	902	2	Q756N1_ASHGO	0756n1 ashbya goss	Q5kqu9 ..	1042	2	
614	34	60.7	905	2	Q4RTX3_TESTING	04rtx3 testing	Q5kqu9 ..	1042	2	
615	34	60.7	907	2	Q87W28_PESM	087w28 pesm	Q5kqu9 ..	1042	2	

689	33	58.9	183	2	Q9Y9G7_AERPE	Q8gmc6_STRLI	Q9y9g7 aeropyrum p	P71615 MYCTU
690	33	58.9	184	2	Q9CRM7_MOUSE	Q9crh7_mus	Q9crh7 mycobacteri	Q7txq9_MYCBO
691	33	58.9	186	2	Q9YR_MTCXE	Q9crh7_mus	Q9crh7 mycobacteri	Q61815_CABBR
692	33	58.9	189	1	OXYR_HUMAN	Q87883_myco	O4lqr3_burkholderi	Q4lqr3_9BURK
693	33	58.9	190	2	Q5WU9_HUMAN	Q5jw9_homo_sapien	Q7we88 bordetella	Q7we88_bordetella
694	33	58.9	191	1	MOBA_PSEPU	Q5jw9_homo_sapien	Q4lv03_burkholderi	Q4lv03_burkholderi
695	33	58.9	191	1	MOBA_PSEPU	Q9wwyo_pseudomonas	Q6tg14_burchydano	Q6tg14_burchydano
696	33	58.9	191	2	Q6TH18_DROME	Q6th18_drosophila	Q4lm86_burkholderi	Q4lm86_burkholderi
697	33	58.9	196	2	Q569A3_RAT	Q569a3_rattus_norv	Q815m8_PLAFT	Q815m8_Plasmid
698	33	58.9	197	1	QENUJ2_HUMAN	Q6mu2_homo_sapien	Q9pt7n6_SCHPO	Q9pt7n6_schizosacch
699	33	58.9	197	2	Q5RC10_PONY	Q5rc10_pongo_pygma	Q67213_crenopharyn	Q67213_crenopharyn
700	33	58.9	197	2	Q5BGK9_MACFA	Q5bgk9_macaca_fasc	Q9W7C4_CYPCA	Q9W7C4_cyprinidae
701	33	58.9	198	1	MOBA_PIEAE	Q68799_pseudomonas	Q91xas_mus_musculus	Q91xas_mus_musculus
702	33	58.9	201	1	MOBA_PSESM	Q883k6_pseudomonas	Q9h715_HUMAN	Q9h715_homo_sapien
703	33	58.9	202	1	DIPA_HUMAN	Q15834_homo_sapien	Q8gt57_CUCHMA	Q8gt57_cucurbita_m
704	33	58.9	202	1	DIPA_MOUSE	Q6pdyo_mus_musculus	Q4sj67_TETING	Q4sj67_tetradon_n
705	33	58.9	202	1	Q96HA0_HUMAN	Q96ha0_homo_sapien	Q8twg7_WHEAT	Q8twg7_wheat
706	33	58.9	203	2	Q5JWA8_HUMAN	Q5jwa8_homo_sapien	Q6l2h1_PICHO	Q6l2h1_picophilus
707	33	58.9	208	2	Q5JWA7_HUMAN	Q5jwa7_homo_sapien	Q82916_STRAW	Q82916_streptomyces
708	33	58.9	209	2	Q5K8B2_CRYNE	Q5kb2_cryptococcus	Q6ke81_secalis_cere	Q6ke81_secale_cere
709	33	58.9	209	2	Q5J9L1_PANTR	Q5j9l1_pan_troglodytes	Q8gvz4_ORYSA	Q8gvz4_oryza_sativa
710	33	58.9	213	2	Q5WT61_9TREM	Q6wt61_nanophytes	Q8h018_ORYSA	Q8h018_oryza_sativa
711	33	58.9	214	2	Q8CC42_MOUSE	Q8cc42_mus_musculus	Q56tko_HUMAN	Q56tko_homo_sapien
712	33	58.9	224	2	Q55MG0_CRYNE	Q55mg0_cryptococcus	Q5b2q5_aspergillus	Q5b2q5_aspergillus
713	33	58.9	224	2	Q5MMN3_CRYNE	Q55mn3_cryptococcus	Q4rx641_maackia_fasc	Q4rx641_maackia_fasc
714	33	58.9	224	2	Q5KEB08_CRYNE	Q5kb08_cryptococcus	Q6dfewo_mus_musculus	Q6dfewo_mus_musculus
715	33	58.9	253	1	UNG_XYLTA	Q9pa28_xylorella_fab	Q75866_homo_sapien	Q75866_homo_sapien
716	33	58.9	253	1	UNG_XYLIFT	Q879z0_xylorella_fab	Q8h930_ORYSA	Q8h930_oryza_sativa
717	33	58.9	255	1	Q55XQ9_CRYNE	Q55xq9_cryptococcus	Q9vqz7_MEETKA	Q9vqz7_meetka
718	33	58.9	255	2	Q7NSBS2_CHRVO	Q7nsb2_chromobacter	Q4v4k2_DROME	Q4v4k2_dromophila
719	33	58.9	257	2	Q7NCX6_GLOVI	Q7ncx6_globobacter	Q5b55se_EMENI	Q5b55se_emeni
720	33	58.9	262	2	Q53MM1_ORYSA	Q53mm1_orzya_sativ	Q8wwf5_HUMAN	Q8wwf5_homo_sapien
721	33	58.9	266	1	Q7XB61_ORYSA	Q7xb61_orzya_sativ	Q7102_MOUSE	Q7102_mouse
722	33	58.9	269	1	SURE_PROM	Q7v8i0_promocili	Q75867_HUMAN	Q75867_homo_sapien
723	33	58.9	270	2	Q5VQ10_ORYSA	Q5vq10_cryptococcus	Q7nzc1_CEPAC	Q7nzc1_chromobacte
724	33	58.9	271	2	Q4hz220_GIBZEE	Q4hz220_gibberella	Q5knz1_CRYNE	Q5knz1_cryptococcus
725	33	58.9	272	2	QSYZ19_ORYSA	Q6yz19_orzya_sativ	Q9vqz7_DROME	Q9vqz7_dromophila
726	33	58.9	274	1	SCP_FETCA	P79169_felis_silvestris	Q4vbz3_HUMAN	Q4vbz3_homo_sapien
727	33	58.9	275	2	Q4WQP3_ASPPU	Q7wbf3_aspergillus	Q7z39_TETNG	Q7z39_tetradon_n
728	33	58.9	279	2	Q726A9_DBSPH	Q726a9_desulfovibr	Q59113_CEPAC	Q59113_cepac
729	33	58.9	289	2	Q5FLD8_CRYNE	Q55ld8_cryptococcus	Q7z739_ORYSA	Q7z739_oryza_sativa
730	33	58.9	289	2	Q5KA0_CRYNE	Q5ka0_cryptococcus	P08039_ANOCLE	P08039_anoploaste
731	33	58.9	290	2	Q5KA16_CHRVO	Q7nb16_chromobacter	P09480_9TELN	P09480_hoplodesthu
732	33	58.9	291	2	Q7WBFF9_BORPA	Q7wbff9_bordetella	P076dt1_PEA	P076dt1_brachydano
733	33	58.9	291	2	Q7WMQ10_BORBR	Q7wmq10_bordetella	P042907_SCHPO	P042907_schizosacch
734	33	58.9	292	2	Q5VQK9_ORYSA	Q5vqk9_orzya_sativ	Q4vys8_KLETING	Q4vys8_kletting
735	33	58.9	294	2	Q9Xd42_AERPE	Q9yd42_aeropyrum	Q89h18_ORYSA	Q89h18_oryza_sativa
736	33	58.9	296	1	FBX37_HUMAN	Q9hw49_homo_sapien	P04gbu8_electoris_ac	P04gbu8_electrois_ac
737	33	58.9	296	1	FBA37_MOUSE	Q9iw61_mus_musculus	Q96hc3_RALSO	Q96hc3_ralstonia_s
738	33	58.9	298	2	Q4K6W0_PSEPF5	Q4k6w0_pseudomonas	Q8hirs5_anoploaste	Q8hirs5_anoploaste
739	33	58.9	299	2	Q5F6P5_BSPFL	Q69756_pseudomonas	Q26660_STONGYLOC	Q26660_stongyloc
740	33	58.9	309	2	Q4D9Y0_XANCP	Q4upy0_xanthomonas	Q94sg0_hoplodesthu	Q94sg0_hoplodesthu
741	33	58.9	309	2	Q8P4C9_XANCP	Q8p4c9_xanthomonas	P076dt1_PEA	P076dt1_pisum_sativum
742	33	58.9	314	1	OXYR_MTCVA	Q5p6777_myco	Q8nhp7_HUMAN	Q8nhp7_homo_sapien
743	33	58.9	314	1	OXYR_MTCVA	Q5p6778_myco	Q9vc10_DROSEA	Q9vc10_drospohila
744	33	58.9	315	2	QSKF45_CRYNE	Q5kf45_cryptococcus	Q8h2ui_ORYZA	Q8h2ui_oryza_sativa
745	33	58.9	315	2	Q5QTA5_HUMAN	Q5qta5_homo_sapien	Q8n644_homo_sapien	Q8n644_homo_sapien
746	33	58.9	316	2	Q6ZWM4_HUMAN	Q6zw94_homo_sapien	Q4im96_GIBZEE	Q4im96_gibberella
747	33	58.9	316	2	Q66ES38_YUROC	Q6es38_oikopleura	Q4v7r2_XENOPUS	Q4v7r2_xenopus_lae
748	33	58.9	317	2	Q7TMST7_HAEUD	Q7wmb7_haemophilus	Q5ze52_ORYSA	Q5ze52_oryza_sativa
749	33	58.9	317	1	FBX37_HUMAN	Q8pfy9_xanthomonas	Q51vl9_MAGGR	Q51vl9_maggr
750	33	58.9	318	2	Q7D6H2_MYCTU	Q7d6h2_myco	Q8h2ui_BRASSICA	Q8h2ui_brassica
751	33	58.9	318	2	Q741U4_NYCPA	Q741u4_myco	Q8xu10_RALSO	Q8xu10_ralstonia_s
752	33	58.9	319	2	Q4V4A1_DROME	Q4v4a1_drosophila	Q96lt7_HUMAN	Q96lt7_homo_sapien
753	33	58.9	319	2	Q8k3B2_MOUSE	Q8k3b2_mus_musculus	Q96hc3_RALSO	Q96hc3_ralstonia_s
754	33	58.9	324	2	Q4Q9S6_BAT	Q4q9s6_rattus_norvegicus	Q96hc3_RAT	Q96hc3_rat
755	33	58.9	325	2	Q73ZL2_NYCPA	Q73zl2_myco	Q96hc3_RAT	Q96hc3_rat
756	33	58.9	326	2	Q6DB15_BRARE	Q6db15_bordetella	Q8qfm3_BRACHYDANO	Q8qfm3_bachydano
757	33	58.9	327	2	Q8BRJ2_MOUSE	Q8brj2_mus_musculus	Q8qfm3_BRACHYDANO	Q8qfm3_bachydano
758	33	58.9	329	2	Q7U3C2_HUMAN	Q7u3c2_homo_sapien	Q8qfm3_BRACHYDANO	Q8qfm3_bachydano
759	33	58.9	332	2	Q83XN5_STRCT	Q83xn5_streptomyces	Q7zu08_BRARE	Q7zu08_brachydano
760	33	58.9	332	2	Q8OYVO_MOUSE	Q8oyvo_mus_musculus	Q7zu08_BRARE	Q7zu08_brachydano
761	33	58.9	334	1	ARGC_BUCAI	P57156_buchnera_ap	Q8qfm3_BRACHYDANO	Q8qfm3_bachydano

835	558	2	Q5V8Z0_HUMAN	homo sapien
836	559	2	Q86NRI_ DROME	drosophila
837	559	2	Q8CDF7_MOUSE	mus musculus
838	594	2	Q52R9_MAGGR	magnaporthe
839	607	2	Q4T7U5_TETNG	tetradocia n
840	608	2	Q61RS4_CAEVR	caenorhabdi
841	616	2	Q9T7O3_CRSB	ceratophyell
842	618	2	Q9T7O4_CERDE	ceratophyell
843	619	2	Q8BH13_SEION	shewanella
844	622	2	Q59EV4_HUMAN	homo sapien
845	623	2	Q66659_9GAMA	equid herpe
846	628	2	Q8R1V5_MOUSE	mus musculus
847	634	2	Q511O7_MAGGR	magnaporthe
848	635	1	LRFN4_HUMAN	homo sapien
849	635	33	Q5KTP9_OREMO	oreochromis
850	649	2	Q4T820_TETNG	tetradocia n
851	655	1	NDC1_YEAST	uvel_neocr
852	656	33	Q9ABD2_STPRGN	strepococc
853	657	2	Q7S2T6_NEUCR	neurospora
854	667	2	Q9ITW4_DROME	drosophila
855	668	33	YFCK_EC057	escherichia
856	668	33	P77182_ecoli	escherichia
857	668	1	YPCK_SHIP1	shigella fl
858	682	33	Q9eau2	zea mays (m
859	693	33	Q945C6_MAIZE	zea mays (m
860	712	2	Q4INP1_GBZB	gibberella
861	714	2	Q8D0B1_YERSINIA	yersinia pe
862	726	2	Q74163_YERPE	yersinia pe
863	726	33	Q6YX06_ORYSA	oryza sativ
864	730	2	CT158_HUMAN	homo sapien
865	730	2	Q945C6_MAIZE	zea mays (m
866	730	2	Q6JDP2_XENLA	xenopus lae
867	730	2	P96436_rhizobium	rhizobium m
868	726	2	Q90ZP4_ONCORHYNCHU	oncorhynchus
869	729	2	Q6YX06_ORYSA	oryza sativ
870	730	2	Q5ND07_GAMAF	gambusia af
871	730	2	Q5F2Z9_CHICK	gallus gallus
872	730	2	Q83DA5_COXBUT	cobia lla bu
873	730	2	Q6JDP2_XENLA	xenopus lae
874	730	2	P96436_rhizobium	rhizobium m
875	752	2	Q90ZP4_ONCORHYNCHU	oncorhynchus
876	755	2	Q6YX06_ORYSA	oryza sativ
877	755	2	Q4P672_USTIMA	ustilago ma
878	765	2	Q7SHZ6_NEUCR	neurospora
879	772	33	Q8ASU2_BACTIN	bacteroides
880	794	2	Q5RCM2_PONPY	pongo pygma
881	835	2	Q86v20_HUMAN	homo sapien
882	851	2	Q7SB82_GAMAP	gambusia af
883	890	2	Q4P672_USTIMA	ustilago ma
884	891	2	Q8ASU2_BACTIN	bacteroides
885	893	2	Q5RCM2_PONPY	pongo pygma
886	894	2	Q57K27_9TRYP	trypanosoma
887	894	33	Q86f23_YARLI	yarrowia li
888	927	2	Q628Y2_ORYSA	oryza sativ
889	931	2	Q8nf26_HUMAN	homo sapien
890	947	1	MUSK_CHICK	mus musculus
891	993	2	Q8ASU2_BACTIN	bacteroides
892	904	2	Q5RCM2_PONPY	pongo pygma
893	935	2	Q86f23_YARLI	yarrowia li
894	951	2	Q628Y2_ORYSA	oryza sativ
895	951	2	Q7SHZ6_NEUCR	neurospora
896	993	2	Q8ASU2_BACTIN	bacteroides
897	904	2	Q57K27_9TRYP	trypanosoma
898	916	2	Q628Y2_ORYSA	oryza sativ
899	927	2	Q8nf26_HUMAN	homo sapien
900	931	2	Q628Y2_ORYSA	oryza sativ
901	949	1	MUSK_CHICK	mus musculus
902	993	2	Q5RCM2_PONPY	pongo pygma
903	1031	2	Q57K27_9TRYP	trypanosoma
904	1042	1	CORIN_HUMAN	homo sapien
905	1042	2	Q4QD82_PLABE	leishmania
906	1047	2	Q4QD82_PLABE	leishmania
907	1047	2	Q4QD82_PLABE	leishmania
908	1047	2	Q4QD82_PLABE	leishmania
909	1049	2	Q4QD82_PLABE	leishmania
910	1049	2	Q4QD82_PLABE	leishmania
911	1058	1	GEM14_RAT	rattus norvegicus
912	1058	1	KCRP_STRPU	streptomyces
913	1058	1	KCRP_STRPU	streptomyces
914	1058	1	KCRP_STRPU	streptomyces
915	1058	1	KCRP_STRPU	streptomyces
916	1058	2	Q4VXV9_HUMAN	homo sapien
917	1058	2	Q4VXV9_HUMAN	homo sapien
918	1058	2	Q4VXV9_HUMAN	homo sapien
919	1058	2	Q4VXV9_HUMAN	homo sapien
920	1058	2	Q4VXV9_HUMAN	homo sapien
921	1058	2	Q4VXV9_HUMAN	homo sapien
922	1058	2	Q4VXV9_HUMAN	homo sapien
923	1058	2	Q4VXV9_HUMAN	homo sapien
924	1058	2	Q4VXV9_HUMAN	homo sapien
925	1058	2	Q4VXV9_HUMAN	homo sapien
926	1058	2	Q4VXV9_HUMAN	homo sapien
927	1058	2	Q4VXV9_HUMAN	homo sapien
928	1058	2	Q4VXV9_HUMAN	homo sapien
929	1058	2	Q4VXV9_HUMAN	homo sapien
930	1058	2	Q4VXV9_HUMAN	homo sapien
931	1058	2	Q4VXV9_HUMAN	homo sapien
932	1058	2	Q4VXV9_HUMAN	homo sapien
933	1058	2	Q4VXV9_HUMAN	homo sapien
934	1058	2	Q4VXV9_HUMAN	homo sapien
935	1058	2	Q4VXV9_HUMAN	homo sapien
936	1058	2	Q4VXV9_HUMAN	homo sapien
937	1058	2	Q4VXV9_HUMAN	homo sapien
938	1058	2	Q4VXV9_HUMAN	homo sapien
939	1058	2	Q4VXV9_HUMAN	homo sapien
940	1058	2	Q4VXV9_HUMAN	homo sapien
941	1058	2	Q4VXV9_HUMAN	homo sapien
942	1058	2	Q4VXV9_HUMAN	homo sapien
943	1058	2	Q4VXV9_HUMAN	homo sapien
944	1058	2	Q4VXV9_HUMAN	homo sapien
945	1058	2	Q4VXV9_HUMAN	homo sapien
946	1058	2	Q4VXV9_HUMAN	homo sapien
947	1058	2	Q4VXV9_HUMAN	homo sapien
948	1058	2	Q4VXV9_HUMAN	homo sapien
949	1058	2	Q4VXV9_HUMAN	homo sapien
950	1058	2	Q4VXV9_HUMAN	homo sapien
951	1058	2	Q4VXV9_HUMAN	homo sapien
952	1058	2	Q4VXV9_HUMAN	homo sapien
953	1058	2	Q4VXV9_HUMAN	homo sapien
954	1058	2	Q4VXV9_HUMAN	homo sapien
955	1058	2	Q4VXV9_HUMAN	homo sapien
956	1058	2	Q4VXV9_HUMAN	homo sapien
957	1058	2	Q4VXV9_HUMAN	homo sapien
958	1058	2	Q4VXV9_HUMAN	homo sapien
959	1058	2	Q4VXV9_HUMAN	homo sapien
960	1058	2	Q4VXV9_HUMAN	homo sapien
961	1058	2	Q4VXV9_HUMAN	homo sapien
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963	1058	2	Q4VXV9_HUMAN	homo sapien
964	1058	2	Q4VXV9_HUMAN	homo sapien
965	1058	2	Q4VXV9_HUMAN	homo sapien
966	1058	2	Q4VXV9_HUMAN	homo sapien
967	1058	2	Q4VXV9_HUMAN	homo sapien
968	1058	2	Q4VXV9_HUMAN	homo sapien
969	1058	2	Q4VXV9_HUMAN	homo sapien
970	1058	2	Q4VXV9_HUMAN	homo sapien
971	1058	2	Q4VXV9_HUMAN	homo sapien
972	1058	2	Q4VXV9_HUMAN	homo sapien
973	1058	2	Q4VXV9_HUMAN	homo sapien
974	1058	2	Q4VXV9_HUMAN	homo sapien
975	1058	2	Q4VXV9_HUMAN	homo sapien
976	1058	2	Q4VXV9_HUMAN	homo sapien
977	1058	2	Q4VXV9_HUMAN	homo sapien
978	1058	2	Q4VXV9_HUMAN	homo sapien
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980	1058	2	Q4VXV9_HUMAN	homo sapien
981	1058	2	Q4VXV9_HUMAN	homo sapien
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984	1058	2	Q4VXV9_HUMAN	homo sapien
985	1058	2	Q4VXV9_HUMAN	homo sapien
986	1058	2	Q4VXV9_HUMAN	homo sapien
987	1058	2	Q4VXV9_HUMAN	homo sapien
988	1058	2	Q4VXV9_HUMAN	homo sapien
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999	1058	2	Q4VXV9_HUMAN	homo sapien
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1002	1058	2	Q4VXV9_HUMAN	homo sapien
1003	1058	2	Q4VXV9_HUMAN	homo sapien
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1006	1058	2	Q4VXV9_HUMAN	homo sapien
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1008	1058	2	Q4VXV9_HUMAN	homo sapien
1009	1058	2	Q4VXV9_HUMAN	homo sapien
1010	1058	2	Q4VXV9_HUMAN	homo sapien
1011	1058	2	Q4VXV9_HUMAN	homo sapien
1012	1058	2	Q4VXV9_HUMAN	homo sapien
1013	1058	2	Q4VXV9_HUMAN	homo sapien
1014	1058	2	Q4VXV9_HUMAN	homo sapien
1015	1058	2	Q4VXV9_HUMAN	homo sapien
1016	1058	2	Q4VXV9_HUMAN	homo sapien
1017	1058	2	Q4VXV9_HUMAN	homo sapien
1018	1058	2	Q4VXV9_HUMAN	homo sapien
1019	1058	2	Q4VXV9_HUMAN	homo sapien
1020	1058	2	Q4VXV9_HUMAN	homo sapien
1021	1058	2	Q4VXV9_HUMAN	homo sapien
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1023	1058	2	Q4VXV9_HUMAN	homo sapien
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1027	1058	2	Q4VXV9_HUMAN	homo sapien
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1029	1058	2	Q4VXV9_HUMAN	homo sapien
1030	1058	2	Q4VXV9_HUMAN	homo sapien
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1032	1058	2	Q4VXV9_HUMAN	homo sapien
1033	1058	2	Q4VXV9_HUMAN	homo sapien
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1036	1058	2	Q4VXV9_HUMAN	homo sapien
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1042	1058	2	Q4VXV9_HUMAN	homo sapien
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1044	1058	2	Q4VXV9_HUMAN	homo sapien
1045	1058	2	Q4VXV9_HUMAN	homo sapien
1046	1058	2	Q4VXV9_HUMAN	homo sapien
1047	1058	2	Q4VXV9_HUMAN	homo sapien
1048	1058	2	Q4VXV9_HUMAN	homo sapien
1049	1058	2	Q4VXV9_HUMAN	homo sapien
1050	1058	2	Q4VXV9_HUMAN	homo sapien
1051	1058	2	Q4VXV9_HUMAN	homo sapien
1052	1058	2	Q4VXV9_HUMAN	homo sapien
1053	1058	2	Q4VXV9_HUMAN	homo sapien
1054	1058	2	Q4VXV9_HUMAN	homo sapien
1055	1058	2	Q4VXV9_HUMAN	homo sapien
1056	1058	2	Q4VXV9_HUMAN	homo sapien
1057	1058	2	Q4VXV9_HUMAN	homo sapien
1058	1058	2	Q4VXV9_HUMAN	homo sapien
1059	1058	2	Q4VXV9_HUMAN	

981	Q5JKA3	oryza sati
982	Q4SCR1	tebraodon
983	Q83ZB6	terrabacae
984	Q87DNG	xytella fata
985	Q7ZK46	xenopus lae
986	Q6PSS0	homo sapiens
987	Q9BV19	homo sapiens
988	Q6ZR66	homo sapiens
989	Q8PP09	xanthomonas
990	Q73DD7	treponema
991	Q5RB15	pongo pygmaeus
992	Q4RN9	tetraodon
993	Q6ZB3	oryza sati
994	Q93J35	streptomyces
995	Q4VB33	homo sapiens
996	Q7V3Z2	lismnf
997	Q92EW8	listeria
998	Q8Y447	listeria m
999	Q6ATHL	desp
1000	Q5SD84	dicystosell

REALIGNMENTS

**RESULT 1**  
 NCGB2H6\_MOUSE PRELIMINARY; PRT; 222 AA.  
 Q8C2H6\_MOUSE PRELIMINARY;  
 Q8C2H6; Tremble1; 23; Created)  
 01-MAR-2003 (Tremble1; 23; last sequence update)  
 01-MAR-2003 (Tremble1; 23; last annotation update)  
 01-OCT-2003 (Tremble1; 25; last annotation update)  
 Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:EG30021G10 product:thymidylylate synthase, full insert sequence. (Fragment).  
 Name=Tyms;  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomii;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;  
 Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
**NUCLEOTIDE SEQUENCE**  
 STRAIN=NOD; TISSUE=Thymus;  
 MEDLINE=92072523; PubMedId=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 Carninci P., Hayashizaki Y.;  
 "High-efficiency full-length cDNA cloning." ;

[2] NUCLEOTIDE SEQUENCE.  
[2] STRAIN=HOD; TISSUE=Thymus;  
[2] MEDLINE=21085660; PubMed=Medline:11217851; DOI=10.1038/35055500;  
[2] Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
[2] Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
[2] Aizawa K., Izawa M., Niimi K., Miyoshi T., Bono H., Kasukawa T., Yamada I.,  
[2] Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
[2] Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T.,  
[2] Plaischmann P., Gaasterland T., Gissi C., King B., Kochiwa H.,  
[2] Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
[2] Schrimal L.M., Staubli F., Suzuki K.R., Tomita M., Wagner L., Washio T.,  
[2] Sakrai K., Okido T., Furuno M., Aono H., Baldarelli R., Barath G.,  
[2] Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
[2] Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,  
[2] Gatzincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
[2] Lyon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
[2] Nordone P., Ring B., Rodriguez I., Sakabano M., Storch K.-F.,  
[2] Sasaki H., Sato K., Schoenbach C., Suya T., Sakabata Y.,  
[2] Suzuki H., Toyō-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
[2] Wijnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
[2] Hayashizaki Y.;  
[2] "Functional annotation of a full-length mouse cDNA collection.";  
[2] Nature 409:685-690(2001).

RP	NUCLEOTIDE SEQUENCE;
RC	STRAIN=NOD; TISSUE=Thymus;
RA	The RIKEN Genome Exploration Research Group Phase I & II Team,
RA	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs,";
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";
RL	Nature 420:1563-1573 (2002).
RN	[14]
RP	NUCLEOTIDE SEQUENCE,
RC	STRAIN=NOD; TISSUE=Thymus;
RX	MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA	Shibata K., Shihara Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Carninci P., Itoh M., Kojima T., Tashiro H., Itou M., Kitaunai T., Harada A., Hayama M., Nishizawa T., Kashiwagi K., Yamamoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RT	Genome Res. 10:1617-1630 (2000).
RN	[15]
RP	NUCLEOTIDE SEQUENCE,
RC	STRAIN=NOD; TISSUE=Thymus;
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Koijima T., Kondo M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numasaki R., Ohno M., Onsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai N., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Segabe Y., Tagami M., Tagawa A., Takashashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the GenBank/DBJ databases.
RL	-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = CC dihydrofolate + dTMP.
CC	-!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC	-!- SIMILARITY: Belongs to the thymidylate synthase family.
DR	HSSP: AK088606; BAC04050.1; - ; mRNA.
DR	HSSP: P04818; 1HW3.
DR	SMR; QC2H6; 1-222.
DR	MG1; MG1:3878; TymG1:3878;
DR	GO:0008168; F: methyltransferase activity; IEA.
DR	GO:0008168; F: thymidylate synthase activity; IEA.
DR	GO:0004799; F: transferase activity; IEA.
DR	GO:0016740; F: thymidylate synthase; IEA.
DR	GO:0006231; P:dTTP biosynthesis; IEA.
DR	GO:0009165; P:nucleotide biosynthesis; IEA.
DR	InterPro: IPR00398; thymidylat synth.
DR	Pfam: PF00303; Thymidylat synth.
DR	PRINTS; PRO108; THYMDNTASE.
DR	ProDom; P00110; Thymidylat synthase; 1.
DR	PROSITE; PS00091; THYMDYLATE SYNTHASE; 1.
KW	Methyltransferase; Nucleotide biosynthesis; Transferase.
FT	NON TER 1 1
SQ	SEQUENCE 222 AA; 25133 MW; 300157EB7AC78CA5 CRC64;
Query Match	100.0%; Score 56; DB 2; Length 222;
Best Local Similarity	100.0%; Fred. No. 0.11;
Matches	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	LMALPPCHAL 10

98 LMALPPCHAL 107

Db	Q8C2R3_MOUSE PRELIMINARY;	PRT;	222 AA.
<b>RESULT 2</b>			
Q8C2R3	MOUSE PRELIMINARY;		
ID			
AC	(TREMBLrel. 23, Created)		
DT	01-OCT-2003 (TREMBLrel. 23, Last sequence update)		
DE	DB Mus musculus' 2 days neonate thymic cells cDNA, RIKEN full-length enriched library, clone: E43004M05 product: thymidylate synthase, full insert sequence. (Fragment).		
GN	Name="Tyrms";		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC		
OC	Muridae; Murinae; Mus.		
NCBI_TAXID=10090			
RN	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.; RT "High-efficiency full-length cDNA cloning.";		
RL	RT Meth. Enzymol. 303:19-44 (1999).		
RN	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa T., Hara A., Fukunishi Y., Konno J., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasaiwa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Homann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez L., Rodriguez I., Sasak H., Sato K., Schoenbach C., Soya T., Shibusawa Y., Storch K.-P., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.; RT "Functional annotation of a full-length mouse cDNA collection.";		
RA	RT Nature 409:685-690(2001).		
RN	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus;		
RA	RA the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; RL Nature 420:563-573 (2002).		
RN	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RA	Carinici P., Shibata Y., Hayatsu N., Sugahara Y., Shibusawa K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	RT Genome Res. 10:1617-1630 (2000).		
RN	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumida H., Udagawa H., Hikiji K.; RA "Differential alternative splicing expressions of thymidylate synthase		
RN	RN [1]		
RP	RP NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NOD; TISSUE=Thymus; MEDLINE=22952598; PubMed=12706668; DOI=10.1016/S0076-3885(03)00005-3;		
RA	Hiyatomi H., Tanemura H., Iizuka T., Katsumata K., Nagao K., RA		
RA	RA		

isofoms.";

Cancer Lett. 193:127-131(2003).

-1 - CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.

CC -1 - PATHWAY: Deoxyribonucleotide biosynthesis.

CC -1 - SIMILARITY: Belongs to the thymidylate synthase family.

CC EMBL: AB077207; BAB83576.1; -; mRNAs.

DR HSSP: P04818; 1HVV.

DR Q8WYK4; 59-23.0.

DR Ensembl: ENSG00000168900; Homo sapiens.

DR GO: GO:0008168; F-methyltransferase activity; IEA.

DR GO: GO:00016740; F-thymidylate synthase activity; IEA.

DR GO: GO:00066231; P-dTTP biosynthesis; IEA.

DR GO: GO:0009155; P-nucleotide biosynthesis; IEA.

DR InterPro: IPR000398; Thymidylat synth.

DR Pfam: PF00303; Thymidylat synt; 1.

DR PRINTS; PR00108; THYMIDYLATE SYNTHASE.

DR PRODOM; PD001180; Thymidylat synth; 1.

DR PRSITE; PS00091; THYMIDYLATE SYNTHASE; 1.

KW Methyltransferase; Nucleotide biosynthesis; Transferase.

SEQUENCE 230 AA; D09F8316A504A02A CRC64;

Query Match Score 56; DB 2; Length 230;

Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 1 LMALPPCHAL 10

Db 106 LMALPPCHAL 115

RESULT 4

Q8WYK3\_HUMAN PRELIMINARY; PRT; 279 AA.

Q8WYK3\_HUMAN PRELIMINARY; PRT; 279 AA.

AC Q8WYK3; -

AC Q8WYK3; -

AC 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DT Thymidylate synthase.

OS Homo sapiens (Human)

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo.

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo.

OC NCBI\_TaxID=9506;

OX [!]

RRP NUCLEOTIDE SEQUENCE.

RX MEDLINE=12595989; Published=12706889; DOI=10.1.016/S0304-3805(03)00000-0.

RX Hisatomi H., Tanemura H., Tizuka T., Kataumata K., Nagao K., Sumida H., Udagawa H., Hikiji K.; "Differential alternative splicing expressions of thymidylate synthase isoforms"; Cancer Lett. 193:127-131(2003).

RX -1 - SIMILARITY: Belongs to the thymidylate synthase family.

RX EMBL: AB077208; BAB83577.1; -; mRNAs.

DR HSSP; P04818; 1HVV.

DR Q8WYK3; 26-279.

DR Ensembl: ENSG00000176880; Homo sapiens.

DR GO: GO:0008168; F-methyltransferase activity; IEA.

DR GO: GO:0004739; F-thymidylate synthase activity; IEA.

DR GO: GO:00016740; P-tranferase activity; IEA.

DR GO: GO:00066231; P-dTTP biosynthesis; IEA.

DR GO: GO:0009155; P-nucleotide biosynthesis; IEA.

DR InterPro: IPR000398; Thymidylat synth.

DR Pfam: PF00303; Thymidylat sync; 1.

DR PRINTS; PR00108; THYMIDYLATE SYNTHASE.

DR PRODOM; PD001180; Thymidylat synth; 1.

SEQUENCE 279 AA; 31758 MW; 10B3A53DB10AB763 CRC64;

Query Match Score 56; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

ISQ

RESULT 5					
Qy	1 LMALPPCHAL 10 	TSYS_MOUSE	STANDARD;	PRT;	307 AA.
Db	155 LMALPPCHAL 164				
ID	TYSY MOUSE				
AC	P07607;	(Rel. 07, Created)			
DT	01-APR-1988	(Rel. 07, Last sequence update)			
DT	01-APR-1988	(Rel. 47, Last annotation update)			
DT	10-MAY-2005	(Rel. 47, Last annotation update)			
DE	Thymidylate synthase	(EC 2.1.1.45) (TSase).			
GN	Name-Tsys;				
OS	Mus musculus (Mouse)				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii; Muroidea; Muridae; Murinae; Mus.				
OC					
OX	NCBI_TaxID:10090;				
RN	[1] _				
RP	NUCLEOTIDE SEQUENCE.				
RX	Medline=8817453; PubMed=344407;				
RA	Perryman S.M., Rossana C., Deng T., Vanin E.F., Johnson L.F.;				
RT	"Sequence of a cDNA for mouse thymidylate synthase reveals striking similarity with the prokaryotic enzyme.";				
RT	Mol. Biol. Evol. 3:313-321(1986).				
RL	[2]				
RN	RP				
RP	NUCLEOTIDE SEQUENCE.				
RX	Medline=87057259; PubMed=3782103;				
RA	Deng T., Li, D., Jenk C.H., Johnson L.F.;				
RT	"Structure of the gene for mouse thymidylate synthase. Locations of all introns and multiple transcriptional start sites.";				
RT	J. Biol. Chem. 261:16000-16005(1986).				
RL	[3]				
RN	RP				
RP	NUCLEOTIDE SEQUENCE OF 236-265.				
RX	Medline=89128436; PubMed=2915025;				
RA	Deng T., Li Y., Johnson L.F.;				
RT	"Thymidylate synthase gene expression is stimulated by some (but not all) introns.";				
RT	Nucleic Acids Res. 17:665-658(1989).				
CC	- - CATALYTIC ACTIVITY: 5'-10-methyltetrahydrofolate + dUMP = dihydrofolate + dTTP.				
CC	- - PATHWAY: Deoxyribonucleotide biosynthesis.				
CC	- - SUBUNIT: Homodimer.				
CC	- - SIMILARITY: Belongs to the thymidylate synthase family.				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.				
CC	DR	AAA40439_1; mRNA.			
CC	DR	EMBL; M13019; AAA4044_1; ; Genomic_DNA.			
CC	DR	EMBL; J02817; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; M13347; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; M13348; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; M13349; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; M13350; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; M13351; AAA4044_1; ; JOINED; Genomic_DNA.			
CC	DR	EMBL; X14489; CAA32651_1; ; mRNA.			
CC	DR	PIR; A26323; YXMST.			
CC	DR	HSSP; P45352; IRTS.			
CC	DR	SMR; P07607; 21-301.			
CC	DR	Ensembl; ENSMUSG00000025747; Mus musculus.			
CC	DR	DR MG1; MG1_987878; Tynn.			
CC	DR	InterPro; IPR00398; Thymidylat synth.			
CC	DR	Pfam; PF00303; Thymidylat synth.			
CC	DR	PRINTS; PRO108; THYMDNTTHASE.			
CC	DR	ProDom; PD001180; Thymidylat synth.			
CC	DR	PROSITE; PS00091; THYMIDYLATE SYNTHASE_1.			
CC	DR	Protein Transferases; Nucleotide biosynthesis; Transferase.			
CC	DR	KW			
CC	FT	ACT SITE 189 BY Similarity.			

RESULT 6						
SQ	SEQUENCE	307 AA;	34958 MW;	E4930618C487FD5B CRC64;		
Query Match		100.0%	Score 56;	DB 1;	Length	
Best Local Similarity		100.0%	Pred. No. 0.15;	No. 0.	Indel	
Matches 10;		Conservative 0;	Mismatches 0;			
QY	1 LMALPPCHAL 1.0					
Db	183 LMALPPCHAL 192					
RESULTS						
TYSY_RAT						
ID	TYSY RAT	STANDARD;	PRT;	307 AA.		
AC	P45352;					
DP	01-NOV-1995	(Rel. 32, Created)				
DT	01-NOV-1995	(Rel. 32, Last sequence update)				
DT	10-MAY-2005	(Rel. 47, Last annotation update)				
DE	Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).					
GN	Name-Tsysy;					
OS	Rattus norvegicus (Rat).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Muridae; Muridae; Murinae; Rattus.					
NCBI_TAXID	10116;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE,					
RX	Medline=9226450; PubMed=7711067; DOI=10.1016/0167-4781(88)90005-0; Title=Isolation and expression of rat thymidylate synthase c					
RA	Ciesla J., Weiner K.X., Reston J.T., Maley C., P.;					
RA	"Isolation and expression of rat thymidylate synthase c phylogenetic comparison with human and mouse thymidylate synthase."					
RT	biochim. biophys. acta 1261:233-242(1995).					
RL	[2]					
RN	X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).					
RX	Medline=99110611; PubMed=8944005; DOI=10.1021/bj981981kd; Title="Methotrexate inhibits thymidylate synthase in rat hepatocytes"					
RA	sotelo-Mundo R.R., Ciesla J.J., Dzik J.M., Rode W., Maley C., P.;					
RA	"Cryystal structures of rat thymidylate synthase inhibit a potent anticancer drug."					
RT	biochemistry 38:1087-1094 (1999).					
RL	CC -1-CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate dihydrofolate + dTMP.					
CC	-1-PATHWAY: Deoxyribonucleotide biosynthesis.					
CC	-1-SUBUNIT: Homodimer.					
CC	-1-SIMILARITY: Belongs to the thymidylate synthase family.					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and the removed.					
CC	EMBL; L12138; AAA92340.1; -; mRNA.					
DR	PIR; S53715; SS3715.					
DR	1RTS; X-ray; A/B=1-307.					
DR	2TSR; X-ray; A/B/C/D=1-307.					
DR	3R2I; Tysm.					
DR	InterPro; IPR000398; Thymidylate synthase.					
DR	PF00303; Thymidylate synthase.					
DR	PRINTS; PR00108; THYMDNTASE.					
DR	PRODOM; PD001180; Thymidylate synthase.					
PROSITE	PS00051; THYMIDYLATE_SYNTHASE_B; 1.					
KW	3D-structure; Methyltransferase; Nucleotide biosynthesis					
PT	ACT SITE 189 189 By similarity.					
FT	23 23					
FT	HELIIX 24 37					
FT	STRAND 39 41					
FT	STRAND 49 60					
FT	TURN 62 63					
FT	HELIX 75 86					
FT	TURN 87 88					
FT	STRAND 91 91					

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
 RA Saito T., Okazaki Y., Gotobori T., Bono H., Kasuhawa T., Seito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barich G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincovich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Moshima J., Marzarella J., Mombaerts P.,  
 RA Nardone P., Ring B., Rodriguez N., Ringwald M., Rodriguez I.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta Y., Storch K.-P.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wysniewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohfuki S.,  
 RA Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.",  
 RT Nature 409:685-690(2001).  
 RN [3]

RP NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasuhawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suruki H., Yamamoto I., Kyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nomami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Gough J., Jarvis E.D.,  
 RA Grimmond S., Gustincovich S., Hirokawa N., Jackson J.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagai A., Kurochkin I.V., Lee Y., Lehndorff B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzi L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavani W.J., Perteet G.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Seton M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Weis C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Nakazumi N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,  
 RA Miyazaki A., Saito K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.",  
 RN Nature 420:563-573 (2002).  
 RN [4]

RP NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",  
 RL Genes Res. 10:1617-1630(2000).  
 RN [5]

RP NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Kitsumai T., Tashiro H., Itoh M.,  
 RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujimoto S., Inoue K., Togawa M., Ohara E., Watanuki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kiria A., Hayashizaki Y.,  
 RA "RIKEN integrated sequence analysis (RISA) system: 384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.",  
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."; U.S.A. 99:16899-16903 (2002).  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZBCH II;  
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
 RA Strausberg R.;  
 RL SUBLIST=(DEC-2001) to the EMBL/GenBank/DDBJ databases.  
 -I- CATALYTIC ACTIVITY: 5,10-methylentetrahydrofolate + dUMP =  
 CC dihydrofolate + dTMP.  
 CC -I- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR HSSP; P45352; 1RTS.  
 DR SMR; Q8VDV6; 21-301.  
 DR MGI; MG1:98878; TymS.  
 DR GO; GO:0008168; P:methyltransferase activity; IEA.  
 DR GO; GO:0004799; P:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR Inter-Pro; IPR000398; Thymidylat synth.  
 DR Pfam; PF00303; Thymidylat synth\_1.  
 DR PRINTS; PR00108; THYMDNSNTHASE.  
 DR ProdDom; PD001180; Thymidylat synth\_1.  
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE\_1.  
 KW Methyl transferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 307 AA; 34930 MW; 76F97162468FF9D CRC64;  
 Query Match 100.0%; Score 56; DB 2; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 0.15%; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Insertions 0;  
 Qy 1 LMALPPCHAL 10 PRT; 307 AA.  
 Db 183 LMALPPCHAL 192  
 DE Q9DQH1\_MOUSE PRELIMINARY;  
 AC Q9DQH1\_MOUSE PRELIMINARY;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DE Mus musculus 10 days embryo whole body cDNA. RIKEN full-length  
 DB enriched library, clone:2610017G21 product:thymidylate synthase, full  
 DS insert sequence.  
 GN Name-TyMS;  
 OS Mus musculus (Mouse).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10050;  
 RN [1] NUCLEOTIDE SEQUENCE STRAIN=CZBCH II;  
 RC MEDLINE=9279253; PubMed=1049636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P.; Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21085660; PubMed=112117851; DOI=10.1038/35055500;  
 RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;  
 RA Arakawa T.; Hara A.; Furukoshi Y.; Konno H.; Adachi J.; Yamamoto S.;  
 RA Aizawa K.; Izawa M.; Nishii K.; Kiyosawa H.; Kondo S.; Yamamoto K.;  
 RA Saito T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saito R.;  
 RA Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.;  
 RA Fleischmann W.; Gaasterland T.; Gissi C.; King B.; Kochwa H.;  
 RA Kuehl P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.;  
 Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Washio T.;



DR	Ensembl; ENSG000000176890; Homo sapiens.
DR	HGNC; HGNC:12441; TYMS.
DR	H-InvDB; HX0017793; -.
DR	Reactome; P04818; -.
DR	MIM; 188350; -.
DR	GO; GO:0009157; P:deoxyribonucleoside monophosphate biosynthesis; TAS.
DR	GO; GO:0006281; P:DNA repair; NAS.
DR	GO; GO:0006260; P:DNA replication; NAS.
DR	GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . . ; TAS.
DR	GO; GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR	InterPro; IPR000098; Thymidylat synth.
DR	Pfam; PF00303; Thymidylat synth; 1.
DR	PRINTS; PR00108; THYMDNTHSE.
DR	PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
DR	3D-structure; Direct protein sequencing; Methyltransferase;
KW	Nucleotide biosynthesis; Transferase
FT	INIT MET 0 0
FT	ACT SITE 194 194
FT	TURN 28 28
FT	HELIK 29 42
FT	STRAND 44 46
FT	TURN 49 50
FT	STRAND 54 65
FT	TURN 67 68
FT	TURN 74 77
FT	HELIK 80 91
FT	TURN 92 93
FT	STRAND 96 96
FT	HELIX 97 101
FT	TURN 102 104
FT	TURN 107 109
FT	HELIK 110 112
FT	HELIX 114 119
FT	TURN 120 121
FT	TURN 123 124
FT	TURN 127 128
FT	STRAND 129 129
FT	HELIX 134 140
FT	STRAND 141 141
FT	TURN 142 142
FT	TURN 148 149
FT	TURN 153 154
FT	STRAND 157 157
FT	HELIX 159 169
FT	TURN 171 172
FT	TURN 174 175
FT	STRAND 177 179
FT	TURN 183 185
FT	STRAND 186 188
FT	STRAND 195 203
FT	TURN 204 205
FT	STRAND 206 217
FT	TURN 218 220
FT	HELIK 221 239
FT	TURN 240 241
FT	STRAND 243 257
FT	HELIX 258 260
FT	HELIX 261 268
FT	TURN 269 269
FT	STRAND 277 280
FT	HELIX 287 289
FT	HELIX 292 294
FT	STRAND 295 298
SQ	SEQUENCE 312 AA; 35585 MW; A66F0B6D1973AB41 CRC64;
Query Match	100.0% Score 56; DB 1; Length 312;
Best Local Similarity	100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LMALPPCHAL 10
Db	188 LMALPPCHAL 197
RESULT 1.1	
Q53FB7_HUMAN PRELIMINARY;	
ID Q53FB7;	
AC Q53FB7;	
DT 13-SEP-2005 (TREMBLrel. 31, Created)	
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)	
DE Thymidylate synthetase variant (Fragment).	
OS Homo sapiens (Human).	
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE-Small intestine;	
RA Maruyama K.; Sugano S.;	
RT "Oligo-capping : simple method to replace the cap structure of eucaryotic mRNAs with Oligoribonucleotides.";	
RL Gene 138:171-174 (1994).	
RN [2]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE-Small intestine;	
RA Suzuki Y., Yoshimoto K., Maruyama K., Sugano A., Yokoyama S.;	
RA "Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";	
RL Gene 200:149-156 (1997).	
RN [3]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE-Small intestine;	
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;	
RL Submitted (APR-2005) to the ENSEMBL/GenBank/DBJ databases.	
CC -I-CATALYTIC ACTIVITY: 5'-10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.	
CC -I-PATHWAY: Deoxyribonucleotide biosynthesis.	
CC -I-SIMILARITY: Belongs to the thymidylate synthase family.	
DR AR223372; BAD97092.1; - mRNA.	
DR GO; GO:0004799; P:thymidylate synthase activity; IEA.	
DR GO; GO:0006231; P:dUMP biosynthetic process; IEA.	
KW Methylytransferase; Nucleotide biosynthesis; Transferase.	
FT NON-TER 1 1	
SQ SEQUENCE 313 AA; 3517 MW; 4E8797D5133B5B67 CRC64;	
Query Match	100.0% Score 56; DB 2; Length 313;
Best Local Similarity	100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LMALPPCHAL 10
Db	189 LMALPPCHAL 198
RESULT 1.2	
Q53Y97_HUMAN PRELIMINARY;	
ID Q53Y97;	
AC Q53Y97;	
DT 13-SEP-2005 (TREMBLrel. 31, Created)	
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)	
DE Thymidylate synthetase.	
OS Homo sapiens (Human).	
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.;	
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;	
RA "Cloning of human full-length CDSs in BD Creator(TM) System Donor	

RT vector.";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dtMP.  
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL: BT006811; AAP03457.1; -; mRNA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:000231; P:dtMP biosynthesis; IEA.  
 DR Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 313 AA; 35716 MW; 148D37F19915B6A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 13  
 Q6P045\_BRARE PRELIMINARY; PRT; 318 AA.  
 ID Q6P045\_BRARE PRELIMINARY;  
 AC Q7ZU17; PRT; 319 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Tym protein.  
 GN Name=tym;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio;  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PMID=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PMID=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Peingold E.A., Grouse L.H., Schuler G.D.,  
 RA Altenschul S.P., Collins F.S., Wagner K.H., Shemesh C.M.,  
 RA Hopkins R.F., Zeiberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lognelliano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Schein J.E., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Grimwood J., Schatz M.C.,  
 RA Rodriguez A.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Butterfield Y.S.N., Myers R.M., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;

RG NIH MGC Project;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dtMP.  
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL: BC055845; AAH65845.1; -; mRNA.  
 DR HSSP; P00470; IAW.  
 DR ZFIN; ZDB-GENE-040426-59; tyms.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006231; P: dTTP biosynthesis; IEA.  
 DR GO:008165; B:nucleotide biosynthesis; IEA.  
 DR InterPro: IPR00098; Thymidylat synth.; IEA.  
 DR Pfam: PF00303; Thymidylat synt.; 1.  
 DR PRODom: PD001180; Thymidylat synth.; 1.  
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SEQUENCE 319 AA; 36299 MW; ADFA41E1DDF891A CRC54;  
 SQ [1]

Query Match 100.0%; Score 56; DB 2; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 0.15%;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 195 LMALPPCHAL 204

RESULT 15  
 Q9DGHS5\_BRARE PRELIMINARY:  
 ID Q9DGHS5\_BRARE PRELIMINARY: PRT; 319 AA.

AC Q9DGHS5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Thymidylate synthase.  
 Name=tsase; ORFNames=zoc:56165;  
 Brachydanio rerio (Zaribfish) (Danio rerio).  
 OS Brachydanio; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 Cyprinidae; Danio.  
 OX NCBI\_TAXID=7955;

RN NUCLEOTIDE SEQUENCE.  
 RA Gill R.L. Jr.; Warren J.T. Jr.;  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -I- PATHWAY: Deoxyribonucleotide biosynthesis (By similarity).  
 CC -I- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL; AY005004; AAF97476.1; -; mRNA.  
 DR HSSP; B04818; 1H94.  
 DR ZFIN; ZDB-GENE-040426-59; tms.  
 DR GO; GO:0008168; P:methyltransferase activity; IEA.  
 DR GO; GO:0004799; E:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006231; B:dTTP biosynthesis; IEA.  
 DR InterPro; IPR00098; Thymidylat synth.  
 DR Pram; PF00303; Thymidylat synt.; 1.  
 DR PRINTS; PRO00108; THYMIDYLATE SYNTHASE.  
 DR PRODom; PD001180; Thymidylate synth.; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SEQUENCE 319 AA; 36313 MW; E08B155B09DBE1E84\_CRC54;

Query Match 100.0%; Score 56; DB 2; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 0.15%;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 195 LMALPPCHAL 204

RESULT 16  
 TSY\_NEMIMA STANDARD: PRT; 264 AA.  
 ID TSY\_NEMIMA STANDARD: PRT; 264 AA.  
 AC Q9JT57;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 10-MAY-2005 (Rel. 47, Last sequence update)

DR Thymidylate synthase (EC 2.1.1.45) (TSase).  
 GN Nam-thyA; OrderredLocusNames=NMA1963;  
 OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TAXID=65699;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,  
 RA Kleb S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
 RA Jagels K., Leather S., Mungall K.L., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M.,  
 RA Skeilton J.,

RA Whitehead S., Spratt B.G., Barrell B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2291.".  
 RL Nature 404:502-506 (2000).  
 CC -!- FUNCTION: Provides the sole de novo source of dtMP for DNA biosynthesis (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dtMP = dihydrofolate + dtMP.  
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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CC DR EMBL; AL162757; CAB85183.1; -; Genomic\_DNA.  
 DR PIR; A81825; A81825.  
 DR HSSP; P00470; 1TRG.  
 DR SMR; Q9JY72; 1-264.  
 DR HAMAP; MF 00008; -; 1.  
 DR InterPro; IPR000398; Thymidylat\_synth; 1.  
 DR PFam; PF00303; Thymidylat\_synt; 1.  
 DR ProDom; PD001180; Thymidylate synthase; 1.  
 DR PROSITE; PS00091; THYMIDYLATE\_SYNTHASE; 1.  
 DR Complete proteome; Methyltransferase; Nucleotide biosynthesis; KW Transferase.  
 FT ACT SITE 146 146 By similarity.  
 SQ SEQUENCE 264 AA; 30261 MW; 001E15B5SE16BPC CRC64;  
 Best Local Similarity 100.0%; Pred. No. 0.63; Score 52; DB 1; Length 264;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 141 MALPPCHAL 149

RESULT 19

	TYSY_PSEAE	STANDARD	PRT	264 AA.
ID	-TYSY_PSEAE			
AC	Q916F1;			
DT	28-FEB-2003 (Rel. 41; Created)			
DT	28-FEB-2003 (Rel. 41; Last sequence update)			
DE	Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).			
GN	Name=thyA; OrderedLocusNames=PA0342;			
OS	<i>Pseudomonas aeruginosa</i> .			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.			
OX	NCBI_TaxID=287;			
RN	LARGE SCALE GENOMIC DNA].			
RC	STRAIN=ATCC 15692 / PA01; PMID=10984043; DOI=10.1136/35020399;			
RX	Medline=20437337; Pubmed=10984043; PMID=10984043; DOI=10.1136/35020399;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.I., Mizoguchi S.D., Warrener P.J., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goitry L., Tolentino E.B., Westphal-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.S., Wu Z., Paulsen I.T., Reizer J., Sauer M.H., Jr., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PA01, an opportunistic pathogen.";			
RT	RT			
RA	Hickey B.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Jeffries A.C., Tettelin H., Saunders N.J., Heidelberg J.F., "Complete genome sequence of <i>Neisseria meningitidis</i> (serogroup B).", MEDLINE=10710307; PubMed=10710307; DOI=10.1126/science.287.5459.1809;			
RA	Doddson R.J., Nelson W.C., Gwinn M.J., Debay R.T., Peterson J.D., Hickey B.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T.M., Cleckley A., Blair E., Cittone H., Clark E.B., Cottontree M.D., Utterback T.R., Khoury H.M., Qin H., Vanathavan J.J., Gill J., Scarlato V., Masiognani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Ventier J.C., "Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58.", MEDLINE=287.1809-1815(2000); PubMed=287.1809-1815(2000); DOI=10.1126/science.287.5459.1809;			
RL	Provides the sole de novo source of dtMP for DNA biosynthesis (By similarity).			
CC	-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dtMP = dihydrofolate + dtMP.			
CC	-!- PATHWAY: Deoxyribonucleotide biosynthesis.			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- SIMILARITY: Belongs to the thymidylate synthase family.			

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Matches	9 ; Conservative	0 ; Mismatches	0 ; Indels	0 ; Gaps	0 ;
/	2 MALPPICHAL 10				
\	141 MALPPICHAL 149				

EMBL; AE004472; AUG03731.1; - ; Genomic\_DNA.  
 PIR; DB36002.  
 HSSP; P00470; ITRG.  
 HAMAP; MP\_00008; - ; 1.  
 InterPro; IPR00398; Thymidylat\_synth.  
 PFAM; PF00303; Thymidylat\_synth\_1.  
 PRINTS; PR00108; THYMDNTHASE.  
 PRODOM; PD001180; Thymidylat\_synth; 1.  
 PROSITE; PS00091; THYMIDYLATE\_SYNTHASE; 1.  
 Complete proteome; Methyltransferase; Nucleotide biosynthesis; Transferase.  
 ACT\_SRRP; 146 By similarity;  
 SEQUENCE; 264 AA; 30016 MW; D34075691D06F352 CRC64;  
 RESULT 21  
 TYSY\_NEIGO STANDARD; PRT;  
 ID TYSY\_NEIGO  
 AC O33.80;  
 DT 30-MAY-2000 (Rel. 39, Created).  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DN Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 Name=ThyA;  
 OS Neisseria gonorrhoeae.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 NCBI\_TaxID=485;  
 OC

Query Match 92.9%; Score 52; DB 1; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 0.63;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 STRAIN=MS11;  
 RC  
 MEDLINE=97372537; PubMed=9228757; DOI=10.1016/S0378-1097(97)00164-X;  
 RA Carlson J.H., Hill S.A.;  
 RA "Identification and characterization of thymidylate synthase from  
 RT Neisseria gonorrhoeae."  
 RT Drosophila melanogaster.  
 RT 151.225-220/11997  
 RT

CC -!- FUNCTION: Provides the sole de novo source of dUMP for DNA  
 biosynthesis (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + DUMP =  
 CC -!- dihydrofolate + dTMP.  
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

NCBI\_TaxID=42221;

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 Lewis L.A., Gillaspy C., McLaughlin C., Gipson M., Ducey T.F., Ownbey T., Hartman K., Nyick C., Carson M.B., Vaughn J.J., Thomson C., Song L., Lin S., Yuan X., Najar F., Zhan M., Ren Q., Zhu H., Qi S., Kenton S.M., Lai H., White J.D., Clifton S., Roe A., Dyer D.W.; "The complete genome sequence of Neisseria Gonorrhoeae." Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 -!- CATALYTIC ACTIVITY: 5,10-methyl-4-enyl tetrahydrofolate + dUMP = dihydrofolate + dTMP.  
 -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 -!- SIMILARITY: Belongs to the thymidylate synthase family.  
 EMBL; AE001969; AAW0005.1; -!- Genomic DNA.

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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

2 MALPPCHAL 10
/
142 MALPPCHAL 150

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PRINTS; PR0108; THYMDNTTHASE.
PRODom; P0001180; Thymidylate synthase; 1.
PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
Complete protease; Methyltransferase; Nucleotide biosynthesis;
Transferase.
SEQUENCE 264 AA; 30247 MW; 52A7581DD479781 CRC64;
Query, Match 92.9%; Score 52; DB 2; Length 264;
RESULT 22
TSYB_BIFLO STANDARD; PRT; 266 AA.
ID TSYB_BIFLO
AC Q8G3T9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last BLAST update)
DT 10-MAY-2005 (Rel. 47, Last PDB update)
DT 10-MAY-2005 (Rel. 47, Last RCSB update)
DT 10-MAY-2005 (Rel. 47, Last PDBsum update)
DT 10-MAY-2005 (Rel. 47, Last UniProtKB update)
DT 10-MAY-2005 (Rel. 47, Last UniProtKB-Swiss-Prot update)
DT 10-MAY-2005 (Rel. 47, Last UniProtKB-Swiss-Prot update)

```

GN Name=thmA; OrderedLocusName=BL1665;  
 OS Bifidobacterium longum.  
 OC Bacteria; Actinobacteridae; Bifidobacteriales;  
 NCBI\_TaxID:216816;  
 OX Bifidobacteriaceae; Bifidobacterium.  
 RN [1] NUCLEOTIDE-SEQUENCE [LARGE SCALE GENOMIC DNA].  
 STRAIN=NCNC 2705;  
 MEDLINE=2294977; PubMed=12381787; DOI=10.1073/pnas.212252799;  
 RA Schein M.A., Kamirnowa M., Snel B., Vilanova D., Berger B.,  
 Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,  
 PRIDMORE R.D., Arigoni F.,  
 RT "The genome sequence of *Bifidobacterium longum* reflects its adaptation  
 to the human gastrointestinal tract."  
 Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
 CC -I- FUNCTION: Provides the sole de novo source of dTMP for DNA  
 biosynthesis (By similarity).  
 CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -I- SUBUNIT: Homodimer (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -I- SIMILARITY: Belongs to the thymidylate synthase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

---

CC DR EMBL; AE014295; ANAN25452.1; -; Genomic\_DNA.  
 HSSP; P00470; IP4F.  
 HAMAP; MF\_00008; \_1.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 PFam; PF00303; Thymidylat\_synt\_1.  
 DR PRINTS; PRO00108; THYMDNSNTHASE.  
 DR ProDom; PD001180; Thymidylat\_synt; 1.  
 PROSITE; PS00094; THYMIDYLATE\_SYNTHASE; 1.  
 DR Complete proteome; Methylenetetrahydrofolate + dUMP =  
 dTMP + dihydrofolate + dTMP.  
 KW Transferase; Nucleotide biosynthesis;  
 PT ACT SITE 149 By similarity.  
 SQ SEQUENCE 266 AA; 30689 MW; B8BD2C4BB9D70 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 0.64%; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Insertions 0; Deletions 0;

Qy 2 MALPPCHAL 10  
 Db 144 MALPPCHAL 152

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RESULT 23  
 ID Q91CH7\_9ALPH PRELIMINARY;  
 AC Q91CH7\_9ALPH PRELIMINARY;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Thymidylate synthase.  
 OS Macropodid herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID:137443;  
 RN NUCLEOTIDE SEQUENCE.  
 RA Mattick J.S.;  
 RA Giuliani S., Smith G.A., Polkinghorne I., Mahony T.J., Young P.,  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -I- SIMILARITY: Belongs to the thymidylate synthase family.

---

DR EMBL; AF188480; AAL14421.1; -; Genomic\_DNA.  
 DR HSSP; P04818; 1HZW.  
 DR SMR; Q91CH7; 30-316.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferease activity; IEA.  
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR00303; Thymidylat\_synt; 1.  
 DR Pfam; PF001180; Thymidylat synth.  
 DR PRINTS; PRO00091; THYMIDYLATE\_SYNTHASE; 1.  
 DR ProDom; PD001180; Thymidylate synthase.  
 DR PROSITE; PS00091; THYMIDYLATE\_SYNTHASE; 1.  
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 316 AA; 35931 MW; 6241CD87DA4AD0B CRC64;

Query Match 92.9%; Score 52; DB 2; Length 316;  
 Best Local Similarity 90.0%; Pred. No. 0.75%;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 192 LMALPPCHAL 201

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RESULT 24  
 ID Q9E202\_9ALPH PRELIMINARY;  
 PRTR; 295 AA.  
 DR Q9E202\_9ALPH PRELIMINARY;  
 ID Q9E202;  
 AC Q9E202;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Thymidylate synthase (EC 2.1.1.45) (TS) (TSbase).  
 OS Cercoptilomec herpesvirus 9 (Simian varicella virus).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID:35246;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21251382; PubMed=11352672; DOI=10.1006/viro.2001.0912;  
 RA Gray W.L., Starnes B., White M.W., Mahalingam R.;  
 RT "The DNA sequence of the simian varicella virus genome."  
 RL Virology 284:123-130 (2001).

Query Match 92.9%; Score 52; DB 1; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 0.64%; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Insertions 0; Deletions 0;

Qy 2 MALPPCHAL 10  
 Db 144 MALPPCHAL 152

---

RESULT 25  
 ID Q91CH7\_9ALPH PRELIMINARY;  
 AC Q91CH7\_9ALPH PRELIMINARY;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Thymidylate synthase.  
 OS Macropodid herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID:137443;  
 RN NUCLEOTIDE SEQUENCE.  
 RA Mattick J.S.;  
 RA Giuliani S., Smith G.A., Polkinghorne I., Mahony T.J., Young P.,  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -I- SIMILARITY: Belongs to the thymidylate synthase family.

Db 171 LMALPPCHML 180

RESULT 25				
TYSY_HHV8	STANDARD;	PRT;	337 AA.	
ID P90463	39, Created			
AC				
DT 30-MAY-2000	(Rel. 39, Last sequence update)			
DT 30-MAY-2000	(Rel. 39, Last annotation update)			
DB TYSY_HHV8	Thymidylate synthase (EC 2.1.1.45) (TS) (TSSe)			
GN Name="thya"; Order=editLocusName=CV1027;..	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC Chromobacterium violaceum.	Neisseriaceae; Chromobacterium.			
OC NCBITaxonID=536;				
RN [1]				
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC STRAIN=ATCC 12472 / DSM 30191;				
RC MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1882124100;				
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,				
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,				
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,				
RA Astolfi-Piho S., Azevedo V., Baptista A.J., Bataus L.A.M.,				
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,				
RA Bordignon J., Brígido M.M., Brito C.A., Broccolini M., Buriti H.A.,				
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,				
RA Carvalho C.M.B., Cassardo J.C.M., Cavada B.S., Chueire L.M.O.,				
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,				
RA Faninatti P., Farías I.P., Ferro J.P., Ferro J.A.,				
RA Ferro M.I.R., Franco G.R., Freitas N.S.A., Furian L.R.,				
RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,				
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,				
RA Leo L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,				
RA Madeira H.M.F., Mantio G.P., Maranhão A.Q., Martins W.S.,				
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,				
RA Nascimento P.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,				
RA Paixao R.F.C., Parente P.O., Pena S.D.J., Pereira J.O.,				
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,				
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,				
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,				
RA Santos E.B.P., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,				
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,				
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmeny T.,				
RA Vettore A., Wasseb R., Zahra A., Simpson A.J.G.,				
CC -1- SUBUNIT: Homodimer (By similarity).				
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.				
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.				
CC This Swiss-Prot entry is copyright. It is produced through a collaboration				
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC the European Bioinformatics Institute. There are no restrictions on its				
CC use as long as its content is in no way modified and this statement is not				
CC removed.				
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =				
CC dihydrofolate + dTMP.				
CC -1- SUBPATHWAY: Deoxyribonucleotide biosynthesis.				
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CC the European Bioinformatics Institute. There are no restrictions on its				
CC use as long as its content is in no way modified and this statement is not				
CC removed.				
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DR EMBL: U833348; AAC56948.1; ; Genomic_DNA.				
DR EMBL: U93872; AAC62673.1; ; Genomic_DNA.				
DR EMBL: U71365; AAC34940.1; ; Genomic_DNA.				
DR HSSP; P04818; 1HW4.				
DR InterPro; IPR000398; Thymidylat_synth.				
DR PF00303; Thymidylat_synt_1.				
DR ProDom; PD001180; Thymidylat_synth; 1.				
DR PROSITE; PS00091; THYMIDYLATE_SYNTHASE; 1.				
DR ACT_STRE 219 By similarity.				
DR SEQUNCE 337 AA; 38555 MW; DOEBOE60A3384EC CRC64;				
FT Score 51; DB 1; Length 337;				
KW Methyltransferase; Nucleotide_biosynthesis; Transferase.				
FT ACT_STRE 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
FT SEQUNCE 337 AA; 38555 MW; DOEBOE60A3384EC CRC64;				
Query Match 1 LMALPPCHML 10				
Db 213 LMALPPCHML 222				
RESULT 26				
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ID TYSY_CHRVO				
AC QTNZ95				
DT 10-MAY-2005 (Rel. 47, Created)				
DT 10-MAY-2005 (Rel. 47, Last sequence update)				
DT 10-MAY-2005 (Rel. 47, Last annotation update)				
Qy 2 MALPCHML 10				
Db 141 MALPCHSL 149				

**RESULT 27**

TSY-LISIN	STANDARD;	PRT;	314 AA.
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Q9ZAD;			
AC			
DT 28-FEB-2003 (Rel. 41; Created)	41;	Last sequence update	
DT 28-FEB-2003 (Rel. 41; Last annotation update)			
DT 10-MAY-2005 (Rel. 47; Last annotation update)			
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSbase).			
GN Listeria innocua; OrderedLocusNames=lin1988;			
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.			
OC NCBI_TaxID=1642;			
OX RN [1]			
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RX PubMed=15115801; DOI=10.1093/nar/gkh562;			
RX Nelson K.B., Routs D.E., Mongodin E.F., Ravel J., Debey R.T., Paulsen I.T., RA Kolonay J.P., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T., RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J., RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R., RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N., RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Ulrich G.A., RA Bayles D.O., Luchansky J.B., Fraser C.M., RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogene reveal new insights into the core genome components of this species." ;			
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussargent O., RA Entian K.-D., Pashi H., Garcia-del Portillo F., Garrido P., RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurakapit G., RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H., RA Novelski G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R., RA Remmeli B., Rose M., Schlueter T., Simoes N., Tierrez A., RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; RT Comparative genomics of Listeria species." ;			
RL Science 294:849-852 (2001).			
CC -1- PUNCTION: Provides the sole de novo source of dtMP for DNA			
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dtMP = dihydrofolate + dtMP.			
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.			
CC -1- SUBUNIT: Homodimer (By similarity).			
CC -1- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).			
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.			
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CC -1- SIMILARITY: Belongs to the thymidylate synthase family.			
CC -1- CATALYTIC ACTIVITY: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC DR EMBL; AE017328; AA04673.1; ; Genomic_DNA.			
CC DR HSSP; P00470; IAXW.			
CC DR SMR; Q71Y51; 4-314.			
CC DR TIGR; LM0523365_1904; -.			
CC DR HAMAP; MF_00005; -; 1.			
CC DR InterPro; IPR00398; Thymidylat synth_1.			
CC DR Pfam; PF00303; Thymidylat synth_1.			
CC DR PRINTS; PR00105; THYMDNTHASE.			
CC DR PROSITE; PS00091; THYMIDYLATE SYNTHASE_1.			
CC DR Complete proteome; Methyltransferase; Nucleotide biosynthesis; KW Transferase.			
CC FT ACT SITE 196 196 By similarity.			
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CC DR PIR; AB1681; AB1681.			
CC DR HSSP; P00467; ITSY.			
CC DR ListList; LIN01988.			
CC DR HAMAP; MF_00008; 1.			
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CC DR PRODOM; PD001180; Thymidylat synt_1.			
CC DR PROSITE; PS00091; THYMIDYLATE SYNTHASE_1.			
CC DR Complete proteome; Methyltransferase; Nucleotide biosynthesis; KW Transferase.			
CC FT ACT SITE 196 196 By similarity.			
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CC DR SMR; Q71Y51; 4-314.			
CC DR TIGR; LM0523365_1904; -.			
CC DR HAMAP; MF_00005; -; 1.			
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CC DR HAMAP; MF_00005; -; 1.			
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CC DR Pfam; PF00103; Thymidylat synt_1.			
CC DR PRINTS; PR00108; THYMDNTHASE.			
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CC DR SMR; Q71Y51; 4-314.			
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CC DR HAMAP; MF_00005; -; 1.			
CC DR InterPro; IPR00398; Thymidylat synth.			

NCBI\_TaxID=1639;  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=RGD-e / Serovar 1/2at;  
 RC DOI=10.1128/JVI.77.14.8159-8165.2003;  
 RA Whity D., Stosei A., Ganache C., Papin J., Bosch M., Smith A.,  
 RA Kedes D.H., White G., Kennedy R., Dittmer D.P.;  
 RA "Novel Kaposis's sarcoma-associated herpesvirus homolog in baboons.";  
 RX MEDLINE#21537279; Published: 01-11-2003; DOI=10.1126/science.1063447;  
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,  
 RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,  
 RA Charbit A., Checoulani P., Couve B., Durand A., Dehoux P.,  
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 RA Entian K.-D., Pshihi H., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
 RA Madueno E., Maitourna A., Mata Vicente J., Ng E., Nedjari H.,  
 RA Nordskog G., Novella S., Perez-Diaz J.-C., Purcell R.,  
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 RL Science 294:849-852 (2001).  
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CC DR EMBL; AL591981; CAC99552.1; -; Genomic\_DNA.  
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 DR HSSP; P00467; ITSPY.  
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 DR HAMAP; MF\_00008/-; 1.  
 DR Interpro; IPR000398; Thymidylat Synth.  
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 DR PRODOM; PD001180; Thymidylat synth; 1.  
 DR PROSITE; PS00093; THYMIDYLATE SYNTHASE; 1.  
 DR Complete proteome; Methyltransferase; Nucleotide biosynthesis;  
 DR Transferase.  
 FT ACT SITE 196 196 By similarity.  
 SQ SEQUENCE 314 AA; 36163 MW; 2E8191ABD21ADF15 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 314;  
 Best Local Similarity 88.9%; Pred. No. 2.5%;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 191 MALPPCHSL 199

RESULT 31  
 Q8QYZ3\_RTRV PRELIMINARY;  
 ID Q8QYZ3\_RTRV PRELIMINARY;  
 AC Q8QYZ3;  
 DR 01-JUN-2002 (TREMBLrel. 21, Created)  
 DR 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Thymidylate synthase-like protein.  
 OS Rana tigrina ranavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.  
 OX NCBI\_TaxID=160631;  
 RN [1]\_TAXID=160631;  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE#211876922; PubMed=11876922; DOI=10.1006/viro.2001.1245;  
 RA He J.G., Lu L., Deng M., He H.H., Weng S.P., Wang X.H., Zhou S.Y.,  
 RA Hong Q.X., Wang X.Z., Chan S.M.;  
 RT Sequence analysis of the complete genome of an iridovirus isolated  
 from the tiger frog";  
 RL Virology 292:185-197(2002).  
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL; AF389451; AAL77812.1; -; Genomic\_DNA.  
 DR HSSP; P45352; IRS.  
 DR SMR; Q8QYZ3; 1-124.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.  
 DR GO; GO:0016740; F:transferease activity; IEA.  
 DR GO; GO:0006231; P:dTTP biosynthesis; IEA.  
 DR Interpro; IPR000398; Thymidylat synth.  
 DR Pfam; PF000303; Thymidylat synth; 1.  
 DR PRINTS; PRO0108; THYMDNSYNTHASE.  
 DR PRODOM; PD001180; Thymidylat synth; 1.  
 DR PROSITE; PS00093; THYMIDYLATE SYNTHASE; 1.  
 DR SEQUENCE .124 AA; 14002 MW-.7123A290B15E6D21 CRC64;

Query Match 85.7%; Score 48; DB 2; Length 124;  
 Best Local Similarity 77.8%; Pred. No. 1.5%;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB	Thymidylate synthase (EC 2.1.1.45) (TS) (TSAe); Name=thya; OrderedNames=Rv2764c, MTIV002.29c;	
GN	Mycobacterium tuberculosis, Name=thya; OrderedNames=Rv2764c, MTIV002.29c;	
OS	Mycobacterium tuberculosis, Organism=Mycobacterium tuberculosis;	
OC	Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.	
OC	NCBI_TaxID=1773;	
OX	NCBI_TaxID=1773;	
RY	RESULT 32	
Db	TYSY MYCBO STANDARD; PRT; 263 AA.	
ID	P67045; O33306; STANDARD; PRT; 263 AA.	
AC	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	30-MAY-2005 (Rel. 47, Last annotation update)	
DE	Thymidylate synthase (EC 2.1.1.45) (TS) (TSAe).	
GN	Name=thya; OrderedNames=Mb2764c;	
OS	Mycobacterium bovis.	
OC	Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.	
OC	NCBI_TaxID=1765;	
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RP	STRAIN=AF2122/97; MEDLINE=22709107; PubMed=127688972; DOI=10.1073/pnas.1130426100;	
RX	Garnier T., Biglmaier K., Camus J.C., Medina N., Mansoor H., Poirier M., Duthou S., Grondin C., Lacroix C., Monsempé C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Partille J., Barrell B.G., Cole S.T., Gordon S.V., Hawkinson R.G.; "The complete genome sequence of Mycobacterium bovis"; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).	
RA	-1- FUNCTION: Provides the sole de novo source of dUMP for DNA biosynthesis (By similarity).	
CC	-1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.	
CC	-1- PATHWAY: Deoxyribonucleotide biosynthesis.	
CC	-1- SUBUNIT: Homodimer (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).	
CC	-1- SIMILARITY: Belongs to the thymidylate synthase family.	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is removed.	
CC	EMBL; BX248343; CADD94971.1; -; Genomic_DNA.	
DR	HSSP; P00470; 1TRG.	
DR	HAMAP; MF_00008; '-'; 1.	
DR	InterPro; IPR000398; Thymidylat_synth.	
DR	Pfam; PF00303; Thymidylat_synth_1.	
DR	PRINTS; PR00108; THYMDSTNTHASE.	
DR	ProDom; PD001180; Thymidylat_synth_1.	
DR	PROSITE; PS000901; THYMIDYLATE_SYNTHASE_1.	
KW	Complete proteome; Methyltransferase; Nucleotide biosynthesis; Transferase.	
KW	ACT SITE 146 146 By Similarity.	
FT	ACT SITE 146 146 By Similarity.	
SQ	SEQUENCE 263 AA; 29853 MW; DF48279E3B9EA5F3 CRC64;	
RY	Query Match Score 48; DB 1; Length 263;	
Db	Best Local Similarity 100.0%; Pred. No. 3.1; Mismatches 0; Gaps 0;	
RY	2 MALPPCHA 9	
Db	141 MALPPCHA 148	
RESULT 33	TYSY MYCBO STANDARD; PRT; 263 AA.	
AC	P67045; O33306; STANDARD; PRT; 263 AA.	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DT	10-MAY-2005 (Rel. 47, Last annotation update)	
DB	Query Match Score 48; DB 1; Length 263;	
DB	Best Local Similarity 100.0%; Pred. No. 3.1; Mismatches 0; Gaps 0;	

Db	141	MALPPCH1A	148				
<b>RESULT 34</b>							
TYSB_BACAM	BACAM	STANDARD;	PRT;	264	AA.		
AC P54081;							
DT 01-OCT-1996 (Rel. 34, Created)							
DT 30-MAY-2000 (Rel. 39, Last sequence update)							
DT 13-SEP-2005 (Rel. 48, Last annotation update)							
DB Thymidylate synthase B (EC 2.1.1.45) (TSB) (TSase B).							
GN Name=thyB; Synonyms=thyBA;							
OS Bacillus amyloliquefaciens							
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.							
OX NCBI_TaxID=1390;							
RN [1]							
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].							
RC STRAIN=ATCC 23844;							
RA Steinborn G., Richter K.,							
RT "Cloning of the <i>Bacillus</i> thymidylate synthase genes <i>thyBA</i> and <i>thyBL</i> .";							
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.							
CC -I- FUNCTION: Provides the sole de novo source of dTMP for DNA biosynthesis (By similarity).							
CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.							
CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.							
CC -I- SUBUNIT: Homodimer (By similarity).							
CC -I- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).							
CC -I- SIMILARITY: Belongs to the thymidylate synthase family.							
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.							
CC DR: 250164; CAA090532_1; ALT_INIT; Genomic_DNA.							
DR HSSP; P00470; ITYS.							
DR HAMAP; MF 00008; -; 1.							
DR InterPro: IPR000398; Thymidylat_synth.							
DR Pfam; PF00303; Thymidylat_synt_1.							
DR PRINTS; PT00108; THYMDSYNTASE.							
DR Prod0n; P0001180; Thymidylat_synt_1.							
DR PROSITE; PS00094; THYMIDYLATE_SYNTHAS_E; 1.							
DR Methyltransferase; Multigene family; Nucleotide biosynthesis;							
KW Transferase.							
FT ACT SITE 146 146 By similarity.							
FT SEQUENCE 264 AA; 30350 MW; 3092687D5653105B CRC64;							
Qy Query Match		85.7%	Score 48;	DB 1;	Length 264;		
Best Local Similarity 88.9%;	Pred. No. 3.2;						
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
Qy 2 MALPPCH1A 10							
Db 141 MALPPCH1C 149							
<b>RESULT 35</b>							
TYSB_BACSU	BACSU	STANDARD;	PRT;	264	AA.		
ID TYSB_BACSU							
AC P11074;							
DT 01-JUL-1989 (Rel. 11, Created)							
DT 01-JUL-1989 (Rel. 11, Last sequence update)							
DT 10-MAY-2005 (Rel. 47, Last annotation update)							
DB Thymidylate synthase B (EC 2.1.1.45) (TSB) (TSase B).							
GN Name=thyB; OrderedLocusNames=BsuU21820;							
OS <i>Bacillus subtilis</i> .							
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .							
OX NCBI_TaxID=1423;							
RN [1]							
RP NUCLEOTIDE SEQUENCE.							
RC STRAIN=168;							
RX MEDLINE=88:84366; PubMed=2840350; DOI=10.1016/0378-1119(88)90476-3;							
RA Iwakura M., Kawata M., Tsuda K., Tanaka T.;							
RT "Nucleotide sequence of the thymidylate synthase B and dihydrofolate reductase genes contained in one <i>Bacillus subtilis</i> operon.";							
RL Gene 64:9-20(1988).							
RC STRAIN=168 / Marburg.							
RP NUCLEOTIDE SEQUENCE.							
RC STRAIN=168, and ATCC 6633 / PCI 219;							
RX MEDLINE=96:49105; PubMed=8760912;							
RA Sorokin A.V., Acevedo V., Zumstein B., Galleron N., Ehrlich S.D.,							
RA Serror P.,							
RT "Sequence analysis of the <i>Bacillus subtilis</i> chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome.";							
RL Microbiology 14:2005-2016(1996).							
RN [2]							
RC STRAIN=168 / Marburg.							
RP NUCLEOTIDE SEQUENCE.							
RC STRAIN=168, and ATCC 6633, and ATCC 6633 / PCI 219;							
RX MEDLINE=93:87974; PubMed=8510640;							
RA Montorsi M., Lorenzetti R.,							
RT "Heat-stable and heat-labile thymidylate synthases B of <i>Bacillus</i> subtilis: comparison of the nucleotide and amino acid sequences.";							
RL Mol. Gen. Genet. 239:1-5(1993).							
RN [3]							
RC STRAIN=168 / Marburg.							
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].							
RC STRAIN=168;							
RX MEDLINE=98:44033; PubMed=9384377; DOI=10.1038/36786;							
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G., Borchart S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Brignell S.C., Bron S., Borris R., Bourquier L., Brans A., Braun M., Caldwell B., Caponno V., Carter N.M., Brouillet S., Bruschi C.V., Caldwell B., Codani J.-J., Connerton I.P., Cummings N., Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T., Entian K.-D., Errington J., Fabret C., Ferrari E., Fujita M., Fujita Y., Fumagalli A., Galleron N., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Grandi G., Ghim S.-Y., Glaser P., Goiffeau A., Golightly B.J., Harwood C.R., Henaut A., Giuseppe G., Guy B.J., Halech J., Haga K., Holzapfel S., Hosono S., Hull M.-F., Itaya M., Hilbert H., Holzapfel S., Karamata D., Kasahara Y., Klaarr-Bianchard M., Jones L.-M., Joris B., Kuroda S., Kuroda Y., Kurogi S., Kurogi S., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kuritka K., Lapidus A., Lardinois S., Lauber J., Lazaravic V., Lee S.-M., Levine A., Liu H., Masuda S., Maeli C., Medina C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noon D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadée Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi Y., Seiwakawa A., Seror P., Shin B.-S., Solido B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Togomi A., Tosato V., Uchiyama S., Vandenberg M., Wedler B., Weitzneger T., Wambatt R., Winter P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H., Danchin A., Yoshiba Y., Yutani K.							
RA The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ;							
RL Nature 390:249-256(1997).							
CC -I- FUNCTION: Provides the sole de novo source of dTMP for DNA biosynthesis.							
CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.							
CC -I- BIOPHYSICOCHEMICAL PROPERTIES:							
CC -I- Temperature dependence:							
CC -I- Pathway: Deoxyribonucleotide biosynthesis.							
CC -I- Subunit: Homodimer.							
CC -I- Subcellular location: Cyttoplasmic (By similarity).							
CC -I- Miscellaneous: <i>Cytosolic</i> (By similarity).							
CC -I- Similarity: Belongs to the thymidylate synthase family.							

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RA	MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;			
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Halling C., Mullin L.,			
RA	Quirollo B., Goodman Y., Cao Y., Aszenazi M., Iartchouk O., Epp A., Liu F.,			
RA	Houmiel K., Gordon J., Vaudin M., Doughty D., Scott C., Lappas C., Markez B.,			
RA	Flanagan C., Allinger M., Gurson J., Lomo C., Sear C., Strub G.,			
RA	Cielo C., Slater S.,			
RT	"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";			
RT	Agrobacterium Science 294:2323-2328(2001).			
RL	-!- FUNCTION: Provides the sole de novo source of dTMP for DNA biosynthesis (By similarity).			
CC	-!- CATALYTIC ACTIVITY: 5,10-methylentetrahydrofolate + dUMP = CTHydrofolate + dTMP.			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- PATHWAY: Deoxyribonucleotide biosynthesis.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- SIMILARITY: Belongs to the thymidylate synthase family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-----			
DR	EMBL; AE009155; AAU40391; -!- Genomic DNA.			
DR	EMBL; AB008121; AAK87800; ALT_INIT; Genomic_DNA.			
DR	PIR; AI2827; A12827.			
DR	HSSP; P00470; ITRG.			
DR	HAMAP; MF_000098; 1.			
DR	InterPro; IPR000398; Thymidylat-synth.			
DR	Pfam; PF00103; Thymidylat synt; 1.			
DR	PRINTS; PRO0108; THYMDSYNTHASE.			
DR	ProDom; PD001180; Thymidylat synt; 1.			
DR	PROSITE; PS00091; THYMIDYLATE_SYNTHASE; 1.			
DR	Complete Protease; Methylltransferase; Nucleotide biosynthesis; KW			
FT	ACT SITE 161 AA; 161 MW; By Similarity.			
SQ	SEQUENCE 264 AA; 29875 MW; 9B44EPA6E7D3337 CRC64;			
Qy	2 MALPPCHAL 10			
Db	141 MALPPCHCL 149			
RESULT 37				
RNS	TYSY_BDEBA	STANDARD;	PRT;	264 AA.
RP	ID TYSY_BDEBA			
RC	Q6M1D2;			
AC				
DT	10-MAY-2005 (Rel. 47, Created)			
DT	10-MAY-2005 (Rel. 47, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DB	Thymidylate synthase (EC 2.1.1.15) (TS) (TSAE).			
DN	Name=tbyA; OrderedLocusNames=Bd3230;			
OS	Bdelliovibrio bacteriovorus			
OC	Bdelliovibrionaceae; Deltaproteobacteria; Bdellovibrionales;			
OC	Bdelliovibrio; Proteobacteria; Bdellovibri.			
OX	NCBI_TAXID=959;			
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RP	STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;			
RC	PubMed=14752164; DOI=10.1126/science.1093027;			
RC	Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,			
RA	Keller H., Lambert C., Evans K.J., Schuster S.C.,			
RA	Sackler R.E., Goessmann A., Meyer F.,			
RA	"A predator unmasked: life cycle of Bdelliovibrio bacteriovorus from a genomic perspective."			
RT	Science 303:688-692 (2004).			
CC	-!- FUNCTION: Provides the sole de novo source of dTMP for DNA biosynthesis (By similarity).			

CC biosynthesis (By similarity).  
 CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 CC dihydrofolate + dTMP.  
 CC HSSP; P00470; 1TYS.  
 CC DR HSSP; BA000040; BAC5177.1; -; Genomic\_DNA.  
 CC DR HAMAP; MF\_00008; -; 1.  
 CC DR InterPro; IPR000398; Thymidylat\_synth.  
 CC DR Pfam; PF00103; Thymidylat\_synt\_1.  
 CC DR PRINTS; PRO0108; THYMDYLATE\_SYNTHASE.  
 CC DR ProdDom; PD001180; Thymidylat\_synt\_1.  
 CC DR PROSITE; PS00091; THYMDYLATE\_SYNTHASE; 1.  
 CC KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;  
 CC Transferase.  
 CC FT ACT\_SITE 146 146 By similarity.  
 CC SQ SEQUENCE 264 AA; 29941 MW; 112056CA0989073F CRC64;  
 DR EMBL; BX842655; CAE78047.1; -; Genomic\_DNA.  
 DR HSSP; P00470; 1AXW.  
 DR HAMAP; MF\_00008; -; 1.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR Pfam; PF00103; Thymidylat\_synt\_1.  
 DR PRINTS; PRO0108; THYMDYLATE\_SYNTHASE.  
 DR ProdDom; PD001180; Thymidylat\_synt\_1.  
 DR PROSITE; PS00091; THYMDYLATE\_SYNTHASE; 1.  
 DR KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;  
 DR Transferase.  
 DR FT ACT\_SITE 146 146 By similarity.  
 DR SQ SEQUENCE 264 AA; 30443 MW; 81229428565B102 CRC64;  
 DR HSSP; P00470; 1TYS.  
 DR Query Match 85.7%; Score 48; DB 1; Length 264;  
 DR Best Local Similarity 100.0%; Pred. No. 3.2;  
 DR Matches 8; Conservative 0; Mismatches 0; Gaps 0;  
 DR Qy 2 MALPPCHAL 9  
 DR Db 141 MALPPCHCL 149  
 DR  
 DR RESULT 39  
 DR TYSY\_BRUME STANDARD; PRT; 264 AA.  
 DR ID TYSY\_BRUME  
 DR AC P67042; QBYT137;  
 DR DT 28-FEB-2003 (Rel. 41; Created)  
 DR DT 25-OCT-2004 (Rel. 45; Last sequence update)  
 DR DT 10-MAY-2005 (Rel. 47; Last annotation update)  
 DR DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 DR GN Name=thya; OrderedLocusNames=BME10618;  
 DR OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 DR OC Brucellaceae; Brucellales;  
 DR OX NCBI\_TaxID=29459;  
 DR RN [1]  
 DR RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 DR RC STRAIN=16M / ATCC 23456 / Biotype 1.  
 DR RX MEDLINE=20020109; PubMed=11756588; DOI=10.1073/pnas.221575398;  
 DR RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,  
 DR RA Ivanova N., Anderson I., Bhattacharyya A., Lykoudis A., Reznik G.,  
 DR RA Jablonski L., Larsen N., D'Souza M., Bernai A., Mazur M., Gotsman E.,  
 DR RA Selkov E., Elzler P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 DR RA Haselkorn R., Kyrides N.C., Overbeek R.;  
 DR RT "The genome sequence of the facultative intracellular pathogen  
 DR Brucella melitensis.";  
 DR RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 DR CC FUNCTION: Provides the sole de novo source of dtMP for DNA  
 DR CC biosynthesis (By similarity).  
 DR CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dtUMP =  
 DR CC dihydrofolate + dtMP.  
 DR CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.  
 DR CC -I- SUBUNIT: Homodimer (By similarity).  
 DR CC -I- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).  
 DR CC -I- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR CC  
 DR RESULT 38  
 DR TYSY\_BRAJA STANDARD; PRT; 264 AA.  
 DR ID TYSY\_BRAJA  
 DR AC Q89G35;  
 DR DT 10-MAY-2005 (Rel. 47; Created)  
 DR DT 10-MAY-2005 (Rel. 47; Last sequence update)  
 DR DT 10-MAY-2005 (Rel. 47; Last annotation update)  
 DR DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 DR GN Name=thya; OrderedLocusNames=b16512;  
 DR OS Bradyrhizobium japonicum.  
 DR OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 DR OC Bradyrhizobiaceae; Bradyrhizobium.  
 DR RN NCBI\_TaxID=375;  
 DR RN [1]  
 DR RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 DR RC STRAIN=USDA 110.  
 DR RX MEDLINE=22484998; PubMed=12597275;  
 DR RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 DR RA Sasamoto S., Watanabe A., Idesawa K., Iriuchi M., Kawashima K.,  
 DR RA Kohara M., Matsumoto M., Shimpoo S., Tsuruoka H., Wada T., Yamada M.,  
 DR RA Tabata S.;  
 DR RT "Complete Genomic Sequence of nitrogen-fixing symbiotic bacterium  
 DR Bradyrhizobium japonicum USDA110.";  
 DR RL DNA Res. 9:189-197 (2002).  
 DR CC -I- FUNCTION: Provides the sole de novo source of dtMP for DNA  
 DR CC biosynthesis (By similarity).  
 DR CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dtMP =  
 DR CC dihydrofolate + dtMP.  
 DR CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.  
 DR CC -I- SUBUNIT: Homodimer (By similarity).  
 DR CC -I- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).  
 DR CC -I- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR CC  
 DR This Swiss-Prot entry is copyright. It is produced through a collaboration  
 DR between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 DR the European Bioinformatics Institute. There are no restrictions on its  
 DR use as long as its content is in no way modified and this statement is not  
 DR removed.  
 DR CC  
 DR EMBL; AE009503; AAL51789.1; -; Genomic\_DNA.  
 DR PIR; AB3228; AB3228.  
 DR HSSP; P00470; 1TYS.  
 DR HAMAP; MF\_00008; -; 1.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR PRINTS; PRO0108; THYMDYLATE\_SYNTHASE.  
 DR ProdDom; PD001180; Thymidylat\_synt\_1.  
 DR PROSITE; PS00091; THYMDYLATE\_SYNTHASE; 1.

KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;  
 KW Transferase.  
 FT ACT SITE 146 146 By similarity.  
 SQ SEQUENCE 264 AA; 30330 MW; FECAD558B5EDCAFA CRC64;

Query Match Score 48; DB 1; Length 264;  
 Best Local Similarity 88.9%; Pred. No. 3.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 40  
 TYSY\_RHIO STANDARD; PRT; 264 AA.

Qy 2 MALPPCHAL 10  
 ID TYSY\_BRUSU STANDARD; PRT; 264 AA.  
 AC P67043; QBYI37; DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 GN Name=Thya; OrderedLocusNames=BR1399;  
 OS Brucellales; Proteobacteria; Alpha proteobacteria; Rhizobiales;  
 OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 NCBI\_TaxID=29465;  
 RN [1] RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC MEDLINE=22247711; PubMed=12271122; DOI=10.1073/pnas.192319099;  
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,  
 RA Van Aken S.B., Riedmiller S., Tettelin H., Gill S.R., White O.,  
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M.,  
 RA Fraser C.M.;  
 RT The Brucella suis genome reveals fundamental similarities between  
 animal and plant pathogens and symbionts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA  
 biosynthesis (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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 use as long as its content is in no way modified and this statement is not  
 removed.

CC -!- EMBL; AE014436; AN30312.1; -; Genomic\_DNA.  
 DR HSSP; P00470; ITYS.  
 DR TIGR; BR1399; -.  
 DR HAMAP; MP\_00008; -; 1.  
 DR InterPro; IPR000398; Thymidylat\_synth.  
 DR Pfam; PF00303; Thymidylat\_synt; 1.  
 DR PRINTS; PR00108; THYMDNTTHASE.  
 DR ProDom; PD001180; Thymidylat\_synth; 1.  
 DR PROSITE; PS00091; THYMIDYLATE\_SYNTHASE; 1.  
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;  
 KW Transferase.  
 FT ACT SITE 146 146 By similarity.  
 SQ SEQUENCE 264 AA; 30330 MW; FECAD558B5EDCAFA CRC64;

Query Match Score 48; DB 1; Length 264;  
 Best Local Similarity 88.9%; Pred. No. 3.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 41  
 TYSY\_RHIME STANDARD; PRT; 264 AA.

Qy 2 MALPPCHAL 10  
 ID TYSY\_RHIME STANDARD; PRT; 264 AA.  
 AC Q92N05; DT 28-FEB-2003 (Rel. 41, Created)

DT	28-FEB-2003 (Rel. 41, Last sequence update)	RX PubMed=14704707; DOI=10.1038/nbt923;
DT	10-MAY-2005 (Rel. 47, Last annotation update)	RA Larimer F.W., Chain P., Hauser L., Lamerdin J.B., Malfatti S., Do L., RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., RA Hansen T.E., Bobst C., Torres Y Torres J.L., Perez C., RA Harrison P.H., Gibson J., Harwood C.S.;
GN	Name=thyA; OrderedLocusNames=R02127; ORFNames=SMC01444;	RT "Complete genome sequence of the metabolically versatile
OS	Bacterium meliloti (Sinorhizobium meliloti)	RT photosynthetic bacterium Rhodopseudomonas palustris.";
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;	RL Biotechnol. 22:55-61 (2004).
OC	Rhizobiaceae; Sinorhizobium.	-i- FUNCTION: Provides the sole de novo source of dtMP for DNA biosynthesis (By similarity).
NCBI_TaxID=382;		CC CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	CC -i- PATHWAY: Deoxyribonucleotide biosynthesis.
RC	STRAIN=1021;	CC -i- SUBUNIT: Homodimer (By similarity).
RX	MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;	CC -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
RA	Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeu A., Kahn D., Kiss B., Lelaike V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebaud P., Vandembol M., Weidner S., Galibert F.;	CC -i- SIMILARITY: Belongs to the thymidylate synthase family.
RA	"Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021";	CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
RT	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).	CC EMBL; BX572604; CAA28934.1; -i- Genomic_DNA.
RL	CC -i- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.	DR HSSP; P00470; IAXW.
CC	CC -i- PATHWAY: Deoxyribonucleotide biosynthesis.	DR HAMAP; MF_00008/-; 1.
CC	CC -i- SUBUNIT: Homodimer (By similarity).	DR InterPro; IPR00398; Thymidylat synt; 1.
CC	CC -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	DR PFAM; PF00103; Thymidylat synt; 1.
CC	CC -i- SIMILARITY: Belongs to the thymidylate synthase family.	DR PRINTS; PRO00108; THYMDNTBASE.
CC	CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	DR PRODOM; PD001180; Thymidylat synt; 1.
CC	CC EMBL; AL591789; CAC46706.1; -i- Genomic_DNA.	DR PROSITE; PS00093; THYMIDYLATE SYNTHASE; 1.
CC	DR HSSP; P00470; ITRG.	KW Complete proteome; Methylltransferase; Nucleotide biosynthesis; Transferase.
CC	DR HAMAP; MP_00008/-; 1.	FT ACT SITE 146 146 By similarity.
CC	DR InterPro; IPR00398; Thymidylat synt; 1.	SQ SEQUENCE 264 AA; 29662 MW; C42FEEEDCBFCPAD CRC64;
CC	DR PFAM; PF00103; Thymidylat synt; 1.	Query Match 85.7%; Score 48; DB 1; Length 264;
CC	DR PRINTS; PRO00108; THYMDNTBASE	Best Local Similarity 88.9%; Pred. No 3.2;
CC	DR PRODOM; PD001180; Thymidylat synt; 1.	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC	DR PROSITE; PS00093; THYMIDYLATE SYNTHASE; 1.	Qy 2 MALPPCHAL 10
CC	DR KW Complete proteome; Methylltransferase; Nucleotide biosynthesis; Transferase.	Db 141 MALPPCHCL 149
CC	FT ACT SITE 146 146 By similarity.	RESULT 44
SQ	SQ SEQUENCE 264 AA; 29987 MW; 056C22E2A2281123 CRC64;	Q57CA9_BRUAB
CC	Query Match 85.7%; Score 48; DB 1; Length 264;	ID Q57CA9_BRUAB PRELIMINARY; PRT; 264 AA.
CC	Best Local Similarity 88.9%; Pred. No. 3.2;	AC Q57CA9;
CC	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DT 10-MAY-2005 (T-EMBLrel. 30, Created)
CC		DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
CC		DR 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CC		DR ThyA, thymidylate synthase.
CC		GN Name=thyA; OrderedLocusName=BruAbI_1394;
CC		DB Brucella abortus.
CC		OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC		OC Brucellaceae; Brucella.
CC		OX NCBI_TaxID=235;
CC		RN [1] _
CC		RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC		RC STRAIN=9-941 / Biovar 1;
CC		RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
CC		RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L., Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
CC		RT "Completion of the genome sequence of Brucella abortus and comparison to the highly similar genomes of Brucella melitensis and Brucella suis.";
CC		RL J. Bacteriol. 187:2715-2726 (2005).
CC		-i- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.
CC		-i- PATHWAY: Deoxyribonucleotide biosynthesis.
CC		-i- SIMILARITY: Belongs to the thymidylate synthase family.
CC		EMBL; AE017223; AAC74725.1; -i- Genomic_DNA.
CC		RN [1] _
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	NCBI_TaxID=1076;	RC STRAIN=CGA009 / ATCC BAA-98;



DT 13-SEP-2005 (TrEMBLrel. 31; Last sequence update)  
 DB Thymidylate synthase (EC 2.1.1.45).  
 GN ORFNames=ArthDRAFT\_2512;  
 OS Arthrobacter sp. FB24.  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Microoccineae; Micrococcaceae; Arthrobacter.  
 OX NCBI\_TaxID=290399;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FB24;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Cope Land A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
 RA Hamm N., Israeni S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";  
 RL Submitted [JUN-2005] to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FB24;  
 RG US DOE Joint Genome Institute (PGP-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24."  
 RL Submitted [JUN-2005] to the EMBL/GenBank/DDBJ databases.  
 CC !- CRUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC !- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =  
 dihydrofolate + dTMP.  
 CC !- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC !- SIMILARITY: Belongs to the thymidylate synthase family.  
 DR EMBL: AAHG010000004; PROTEIN: IPR000398; Thymidylat\_synt.  
 DR InterPro; PF00303; Thymidylat\_synt; 1.  
 DR PRINTS; PRO0108; THYMDNTSYNTHASE.  
 DR PRODOM; PD001180; Thymidylat\_synt; 1.  
 DR PSORT; PS00093; Score 48; DB 2; Length 267;  
 DR Methyltransferase; Nucleotide biosynthesis; Transferase.  
 SQ SEQUENCE 267 AA; 30447 MW; 64DEFA588619AC56 CRC64;

Query Match 85.7%; Score 48; DB 2; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OC NCBI\_TaxID=227470;

RN [1]  
 RN [2]

RESULT 49  
 Q76YC2\_9CAUD PRELIMINARY; PRT; 277 AA.  
 ID Q76YC2\_9CAUD PRELIMINARY;  
 AC Q76YC2;  
 DT 05-JUL-2004 (TrEMBLrel. 27; Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27; Last annotation update)  
 DR DTMBL Synthase.  
 DR Bacteriophage Ahel.  
 DR Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 DR NCBI\_TaxID=227470;

RN [1]  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RA Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M.,  
 RA Karam J.D.;  
 RL Submitted [JUL-2003] to the EMBL/GenBank/DDBJ databases.  
 RN [2]

RESULT 48  
 TYSY\_PROAC STANDARD; PRT; 269 AA.  
 ID TYSY\_PROAC  
 AC Q6A7G1;  
 DT 10-MAY-2005 (Rel. 47; Created)  
 DT 10-MAY-2005 (Rel. 47; Last sequence update)  
 DT 10-MAY-2005 (Rel. 47; Last annotation update)  
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 GN Name=Thya; OrderedLocusNames=P0A1672;  
 OS Propionibacter acnes.  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Propionibacteriinae; Propionibacteriaceae; Propionibacterium.  
 OC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RN NCBI\_TaxID=1747;  
 RP STRAIN=KPA171202 / DSM 16379;  
 RX PubMED:15286373; DOI=10.1126/science.1100330;  
 RA Brueggemann H., Henne A., Hoster F., Lieegang H., Wiezer A.,  
 RA Strittmatter A., Hujer S., Dueire P., Gottschalk G.;  
 RT "The complete genome sequence of Propionibacterium acnes, a commensal  
 of human skin.", Science 305:671-673 (2004).  
 CC !- FUNCTION: Provides the sole de novo source of dTMP for DNA  
 CC biosynthesis (By similarity).  
 CC !- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =

CC dihydrofolate + dTMP.  
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC !- SIMILARITY: Belongs to the thymidylate synthase family.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC DR AE017283; AAT83404.1; -; Genomic\_DNA.  
 CC DR HAMAP; MP\_0008; -; 1.  
 CC DR InterPro; IPR000398; Thymidylat\_synt.  
 CC DR Pfam; PF00303; Thymidylat\_synt; 1.  
 CC DR PRINTS; PRO0108; THYMDNTSYNTHASE.  
 CC DR PRODOM; PD001180; Thymidylat\_synt; 1.  
 CC DR PROSITE; PS00093; THYMIDYLATE\_SYNTHASE; 1.  
 CC KW Complete proteome; MethyVitranBerase; Nucleotide biosynthesis;  
 KW Transferase.  
 FT ACT SITE 145 145 By similarity.  
 SQ SEQUENCE 269 AA; 30838 MW; 80AFC40PSB687168 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 269;  
 Best Local Similarity 88.9%; Pred. No. 3.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 MALPCHAL 10  
 Db 140 MALPCHAL 148

RESULT 49  
 Q76YC2\_9CAUD PRELIMINARY; PRT; 277 AA.  
 ID Q76YC2\_9CAUD PRELIMINARY;  
 AC Q76YC2;  
 DT 05-JUL-2004 (TrEMBLrel. 27; Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27; Last annotation update)  
 DR DTMBL Synthase.  
 DR Bacteriophage Ahel.  
 DR Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 DR NCBI\_TaxID=227470;

RN [1]  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RA Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M.,  
 RA Karam J.D.;  
 RL Submitted [JUL-2003] to the EMBL/GenBank/DDBJ databases.  
 RN [2]

RESULT 48  
 TYSY\_PROAC STANDARD; PRT; 269 AA.  
 ID TYSY\_PROAC  
 AC Q6A7G1;  
 DT 10-MAY-2005 (Rel. 47; Created)  
 DT 10-MAY-2005 (Rel. 47; Last sequence update)  
 DT 10-MAY-2005 (Rel. 47; Last annotation update)  
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).  
 GN Name=Thya; OrderedLocusNames=P0A1672;  
 OS Propionibacter acnes.  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Propionibacteriinae; Propionibacteriaceae; Propionibacterium.  
 OC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RN NCBI\_TaxID=1747;  
 RP STRAIN=KPA171202 / DSM 16379;  
 RX PubMED:15286373; DOI=10.1126/science.1100330;  
 RA Brueggemann H., Henne A., Hoster F., Lieegang H., Wiezer A.,  
 RA Strittmatter A., Hujer S., Dueire P., Gottschalk G.;  
 RT "The complete genome sequence of Propionibacterium acnes, a commensal  
 of human skin.", Science 305:671-673 (2004).  
 CC !- FUNCTION: Provides the sole de novo source of dTMP for DNA  
 CC biosynthesis (By similarity).  
 CC !- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =

CC 2 MALPCHAL 10  
 CC 151 MALPCHAL 159

**RESULT 50**

TYSY_CAUCR	STANDARD;	PRT;	279 AA.
ID _TYSY_CAUCR			
AC Q9A610;			
DT 28-FEB-2003 (Rel. 41, Created)			
DT 28-FEB-2003 (Rel. 41, Last sequence update)			
DT 10-MAY-2005 (Rel. 47, Last annotation update)			
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSbase)			
GN Name=thya; OrderedLocusNames=CC2124;			
CAulobacter crescentus.			
OC Bacteria: Proteobacteria; Alphaproteobacteria; Caulobacterales;			
OC Caulobacteraceae; Caulobacter.			
RN NCBI_TAXID=155892;			
[1]			
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC STRAIN=ATCC 19089 / CB15;			
RX MEDLINE=21173638; PubMed=11259647; DOI=10.1073/pnas.061029298;			
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,			
RA Eisen J.A., Heidelberg J.F., Ohta N., Paulsen I.T., Nelson K.E.,			
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,			
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,			
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,			
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,			
RA Brmlaeva M.D., White O., Salzberg S.L., Ventre J.C., Shapiro L.,			
RA Fraser C.M.;			
RT "Complete genome sequence of Caulobacter crescentus.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001)			
-I- CC FUNCTION: Provides the sole de novo source of dTMP for DNA biosynthesis (By similarity).			
-I- CC CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =			
CC dihydrofolate + dTMP.			
CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.			
CC -I- SUBUNIT: Homodimer (By similarity).			
CC -I- SUBCELLULAR LOCALIZATION: Cyttoplasmic (By similarity).			
CC -I- SIMILARITY: Belongs to the thymidylate synthase family.			
CC			
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CC use as long as its content is in no way modified and this statement is not			
CC removed.			
CC			
DR EMBL; AB005885; ARZ24095.1; - ; Genomic_DNA.			
DR PIR; C87512; CB7512.			
DR HSSP; P00470; 1F4G.			
DR TIGR; CC2124; -.			
DR HAMAP; MF 00008; - ; 1.			
DR InterPro; IPR000398; Thymidylat_synth.			
DR Pfam; PF00303; Thymidylat_synt_1.			
DR PRINTS; PR00108; THYMDNTTHASE.			
DR ProDom; PPD001180; Thymidylat_synth; 1.			
DR PROSITE; PS00094; THYMIDYLATE_SYNTHASE; 1.			
KW Complete proteome; Methylenetetrahydrofolate synthase; Nucleotide biosynthesis; Transferase.			
PT ACT SITE 162 162 By Similarity.			
SQ SEQUENCE 279 AA; 31462 MW; 9EEB36984171B2D7 CRC64;			
Qy 2 MAUPPCHAL 10	85.7%	Score 48;	DB 1;
Best Local Similarity 88.9%;	Pred. No. 3.3;	Length 279;	
Matches 8;	Mismatches 0;	Indels 0;	Gaps 0;
Db 157 MAUPPCHAL 165			

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	7 ADI15844	Adi15844 HLA-A2 re Abg20769 Novel hum
2	56	100.0	216	4 ABG0769	Adc56779 Splice va
3	56	100.0	230	7 ADC56779	Adc56779 Splice va
4	56	100.0	279	7 ADC56780	Abp53743 Human thy
5	56	100.0	284	5 ABP5743	Ahw75754 Mutated t
6	56	100.0	313	2 AAW75754	Ahw75758 Mutated t
7	56	100.0	313	2 AAW75758	Ahw75765 Mutated t
8	56	100.0	313	2 AAW75765	Ahw75757 Mutated t
9	56	100.0	313	2 AAW75765	Ahw75768 Mutated t
10	56	100.0	313	2 AAW75766	Ahw75768 Mutated t
11	56	100.0	313	2 AAW75752	Ahw75756 Mutated t
12	56	100.0	313	2 AAW75763	Ahw75763 Mutated t
13	56	100.0	313	2 AAW75764	Ahw75764 Mutated t
14	56	100.0	313	2 AAW75764	Ahw75775 Mutated t
15	56	100.0	313	2 AAW75765	Ahw75766 Mutated t
16	56	100.0	313	2 AAW75762	Ahw75762 Mutated t
17	56	100.0	313	2 AAW75756	Ahw75756 Mutated t
18	56	100.0	313	2 AAW75759	Ahw75759 Mutated t
19	56	100.0	313	2 AAW75767	Ahw75767 Mutated t
20	56	100.0	313	2 AAW75760	Ahw75760 Mutated t
21	56	100.0	313	2 AAW75761	Ahw75761 Mutated t
22	56	100.0	313	2 AAW75753	Ahw75753 Mutated t
23	56	100.0	313	2 ABP53744	Abp53744 Human thy
24	56	100.0	313	5 AAU87071	Aau87071 Human thy

98	47	83.9	323	6	ABU39749	Protein e	Abg25231	Novel hum
99	47	83.9	323	6	ABU22997	Protein e	Abg25233	Novel hum
100	47	83.9	323	6	ABU41484	Protein e	Aau60176	AAU60176
101	47	83.9	608	8	ADS75088	P. falcip	ABM56695	Propionib
102	47	83.9	612	2	AAV17271	N. caninu	ADM94208	Wheat Dio
103	46	82.1	55	7	ADU62279	Epitocic	AAG39112	Arabidops
104	46	82.1	55	9	AEC10937	Enterococ	AAG39111	Arabidops
105	46	82.1	315	6	ABU29298	Protein e	AAG39110	Arabidops
106	46	82.1	315	7	ADU62274	E. faecali	ABG40558	Peptide #
107	46	82.1	315	7	ADU162276	E. faecali	Aam34226	Peptide #
108	46	82.1	315	9	AEC10932	Enterococ	AAM74513	Human bon
109	46	82.1	315	9	AEC10934	Enterococ	AAM61717	Human bra
110	46	82.1	318	6	ABU42652	Protein e	ABG56304	Human liv
111	46	82.1	318	6	ABU42411	Protein e	Aam33030	Peptide #
112	46	82.1	318	6	ABU42887	Protein e	AAM72800	Human bon
113	46	82.1	318	6	ABU43921	Protein e	Aam60182	Human bra
114	46	82.1	318	9	ADW9714	Protein e	Abg54501	Human liv
115	46	82.1	322	5	ABP38349	Staphyloc	ABG42625	Human pep
116	46	82.1	322	6	ABM73020	Staphyloc	AAG13004	Arabidops
117	46	82.1	324	7	ADC96518	E. faeciu	Aag13003	Arabidops
118	46	82.1	325	7	ADP86461	Enterococ	AAG07125	Arabidops
119	45	80.4	142	7	ADT73100	Human cel	ADA55119	Human pro
120	44	78.6	51	8	ADU16623	M. tuberc	AAG07124	Arabidops
121	44	78.6	75	5	ABP05623	Human ORF	ABG40501	Human ORF
122	44	78.6	93	5	ABP34334	Human syn	AAG07123	Arabidops
123	44	78.6	97	8	ADU06835	Cell adhe	AAB18666	A human r
124	44	78.6	116	8	ADU06836	Cell adhe	Abu52774	Human bra
125	44	78.6	119	8	AAV04823	Mycobacte	ABG27392	Novel hum
126	44	78.6	136	5	ABP63828	Human ORF	AAG07124	Arabidops
127	44	78.6	184	2	AAW06581	Mouse uro	AAB55338	Human pro
128	44	78.6	184	2	AAV21547	Mouse uro	Add18574	Human dis
129	44	78.6	184	3	AAV51073	Murine UP	ADO24443	Human PRO
130	44	78.6	184	4	AAG79102	Amino aci	Ado14973	Pseudomon
131	44	78.6	184	4	AAN79166	Human pro	Adi45097	Rice isop
132	44	78.6	184	5	AAU74525	Human uro	AAU83521	Novel hum
133	44	78.6	184	6	ABR48166	Human bla	Aau19213	Human G P
134	44	78.6	184	7	ADN38855	Cancerian	ABP33352	Human ORF
135	44	78.6	196	4	AAM80150	Human pro	Aau63465	Propionib
136	44	78.6	196	4	ABU35270	Protein e	Abm65984	Propionib
137	44	78.6	280	6	ABU17232	Protein e	ABM65223	Propionib
138	44	78.6	282	8	ADL04890	M. catarr	ABP58342	Plant pol
139	44	78.6	286	5	ADP37377	Acinetob	Abb68782	Drosophili
140	44	78.6	315	5	ABP73399	Candida a	Ady09852	Plant ful
141	44	78.6	328	6	ABU36316	Protein e	ABG28659	Novel hum
142	44	78.6	340	5	ADP35279	Yeast smo	ABM88980	Rice abio
143	44	78.6	344	6	ABU20990	Protein e	ADT40977	HSARS vir
144	44	78.6	344	6	ABU226185	Aspergill	ADT38507	HSARS vir
145	43	76.8	52	5	ADB37773	Thymidyl	AEB00352	SARS coro
152	40.5	72.3	218	2	AAW44089	Human sec	AAB25689	Human sec
153	40.5	72.3	218	2	AAV27653	Secreted	ADt40999	HSARS vir
147	43	76.8	264	9	AEB40796	L. pneumo	AdS80414	SARS vir
148	43	76.8	265	9	ABP32879	Human fet	Adt38529	HSARS vir
149	43	76.8	265	9	ABJ25585	Aspergill	ABY03567	SARS 1006
150	40.5	75.0	264	6	ABU32203	Protein e	Ado0181	Human Pri
156	40.5	72.3	277	9	AEP51131	Pseudomon	AAB64316	Drosophili
151	41	73.2	287	6	AUC35594	Protein e	Aag92369	C. glutam
152	40.5	72.3	287	6	ADU51915	Human cyt	Aab25689	Human sec
157	40.5	72.3	542	7	ADC10136	Human NOV	Ady13196	Plant ful
158	40.5	72.3	645	7	ABP00422	Human ORF	Adp29417	Human sec
159	40	71.4	105	105	ABP00422		Abm96510	M. xanthu
160	40	71.4	118	7	ABP37492		Adx89748	Rat frizz
161	40	71.4	226	4	ADM19928	Protein e	Aaw48785	Thyroid p
162	40	71.4	264	6	ADC31835	Protein e	Aaw48784	Thyroid p
163	40	71.4	264	6	ABU34834	Protein e	Adv26102	Human Pri
164	40	71.4	264	6	ABU50438	Protein e	Adg74260	Mouse fri
165	40	71.4	264	6	ABU45233	Protein e	Abu50596	Protein e
166	40	71.4	264	6	ABU27953	Protein e	Adw67514	Mouse GPC
167	40	71.4	264	6	ABU48277	Protein e	Aea55061	Mouse fri
168	40	71.4	265	6	ABM67522	Protein e	Abu12117	Hydroph
169	40	71.4	265	7	ABO63538	Klebsiell	Abu55896	Human pro
170	40	71.4	417	4	ABG25232	Novel hum	Aae34050	F2D1 prot

244	64.3	647	7	ADG74259	Human fri	Abu21303	Protein e	
245	64.3	647	7	ADP65222	Human fri	Aab42530	Human ORF	
246	36	64.3	647	8	ADP22252	Human FZD	ABU22530	Protein e
247	36	64.3	648	8	ADG29693	Human GPC	Abu20292	Protein e
248	36	64.3	648	9	AEB28125	Human fri	Ade14373	Human int
249	36	64.3	666	7	ABM88902	Rice abio	Adc87349	Human GPC
250	36	64.3	681	2	AAM48786	Thyroid p	Aay82741	DNA repli
251	36	64.3	683	4	ADY10945	Plant ful	Aab94230	Human mit
252	36	64.3	689	2	AAW48787	Thyroid p	Aaq68351	Pseudomon
253	36	64.3	784	2	AAW48783	Thyroid p	Ada03123	Nucleotid
254	36	64.3	785	8	ABM83658	Human dia	Abg04091	Housekeep
260	36	64.3	924	2	AAR35445	Human dia	Abg04091	Novel hum
261	36	64.3	933	8	AAR44615	Human dia	Abg19321	Cyclin-de
262	36	64.3	948	2	AAR07733	Human thy	Adn24167	Bacterial
257	36	64.3	852	2	AAW48782	Thyroid p	Abt6949	Novel hum
263	36	64.3	933	2	AAR75689	Human thy	Aae23384	Human int
264	36	64.3	933	7	ADG68732	Human NOV	Adz25408	Bacterial
265	36	64.3	888	8	ADU79002	Human NOV	Adz26174	Bacterial
266	36	64.3	924	2	AAR34636	Human TPO	Adz24427	Bacterial
267	36	64.3	933	8	ADU1768	Human thy	Adz25693	Bacterial
268	36	64.3	933	9	AAR32875	Human TPO	Adz26484	Alpha-iso
269	36	64.3	948	2	AAW48781	Thyroid p	Abm88297	Enzyme
270	36	64.3	956	9	ABM91196	Human hea	Abp60544	Drosophil
271	36	64.3	933	8	ADQ14321	Human thy	Adl91596	Drosophil
272	36	64.3	1222	4	ABP58342	Drosophil	Ado08526	Novel pro
273	36	64.3	4601	4	ABBS9371	Drosophil	Abp43600	Peptide #
274	35	62.5	14	9	AE335162	LPS bindi	Adi27173	Hyperther
275	35	62.5	14	9	AE498781	Human thy	Adi127173	Rat LRP b
276	35	62.5	15	5	AAO18153	LPS bindi	Abp88471	C aulicus
277	35	62.5	24	8	ADU92085	Human sma	Abp88382	Human bon
278	35	62.5	54	4	ABM65776	Brain der	Abp06409	Human ORF
279	35	62.5	6	ABM53295	Propionib	Abm21267	Peptide #	
280	35	62.5	59	5	AAM49806	Human HPD	Adm25528	Human pro
281	35	62.5	67	4	AU049165	Propionib	Adm37494	Peptide #
282	35	62.5	67	6	AU049165	Propionib	Abm26554	Protein e
283	35	62.5	69	5	ABP64191	Propionib	Aam7344	Sequence
284	35	62.5	91	4	ABG02864	Novel hum	Abg64539	Human bra
285	35	62.5	107	4	AAU32636	Novel hum	Abg58976	Human liv
286	35	62.5	114	5	AAO18164	Human sma	Abg46359	Human psp
287	35	62.5	116	6	AAU52367	Propionib	Abm80322	Human pro
288	35	62.5	116	6	ABM48886	Propionib	Aag66845	Human rib
289	35	62.5	129	4	ABP64191	Propionib	Aap60357	Tumor ant
290	35	62.5	134	8	ADT49203	Protein e	Abp60255	Interfero
291	35	62.5	138	4	AAU50183	Oil-assoc	Aao04294	Human pol
292	35	62.5	138	6	ABM46702	Propionib	Abd64204	Human pro
293	35	62.5	151	5	AAG68341	Human gua	Abm04429	Human pro
294	35	62.5	157	6	ADA54939	Human pro	Abm93921	Human pro
295	35	62.5	157	8	ABR48187	Human bla	Aea37059	Human gen
296	35	62.5	158	8	ADP93673	Plant ful	Abq66744	Plant ful
297	35	62.5	159	4	AAM25961	Human pro	Abu19286	Human G p
298	35	62.5	159	8	ADW87789	Human EST	Abp56864	Xenopus C
299	35	62.5	195	6	ADA55707	Human pro	Abc86625	Human GPC
300	35	62.5	196	9	ADY15592	PRO polyP	Adr09671	Human FRI
301	35	62.5	202	9	ADW87786	Human cor	Adv26408	Human Fri
302	35	62.5	215	7	ADM26545	Cancer,an	Adx08394	Novel pro
303	35	62.5	229	4	AAM39526	Hyperther	Aae17485	Human leu
304	35	62.5	252	7	ADY19522	Human pol	Abg7005	Novel num
310	35	62.5	264	8	ADG58746	Human pol	Aae36182	Human CGD
311	35	62.5	281	9	ABG19781	Novel hum	Ado08187	Human Fri
312	35	62.5	281	9	ABM97038	M. xanthu	Adv26408	Human Fri
313	35	62.5	294	7	ADC51446	Interfero	Aae17485	Novel pro
314	35	62.5	298	4	AAM41312	Human pol	Abg69637	Human sec
315	35	62.5	306	7	ABO84010	Pseudomon	Aau83129	Novel sec
316	35	62.5	308	8	ADx69062	Plant ful	Adv26408	Novel sec

390	34	60.7	295	7	ADB85214	Rat chima
391	34	60.7	311	5	AEE23982	Human LP2
392	34	60.7	341	8	ADT57699	Plant pol
393	34	60.7	343	5	ADJ33317	Human pot
394	34	60.7	365	6	ABR37076	Human gen
395	34	60.7	392	7	ADB74461	Mycobacte
396	34	60.7	411	6	ADA54098	Human pro
397	34	60.7	411	7	ADU70680	Human hea
398	34	60.7	425	8	ADM87642	Human EST
399	34	60.7	455	7	ABM89085	Rice abio
400	34	60.7	466	6	ABR58660	Human can
401	34	60.7	467	5	AAO16105	Human act
402	34	60.7	468	7	ADM59897	Human Pro
403	34	60.7	499	8	ADM87184	Human pro
404	34	60.7	512	7	ADM74270	Mouse tri
405	34	60.7	515	7	ABM85921	Rice abio
406	34	60.7	529	5	ABB07502	Human GTP
407	34	60.7	545	6	ABG59976	Human DIT
408	34	60.7	547	4	AAG67550	Amino aci
409	34	60.7	547	8	ADR09923	Human pro
410	34	60.7	572	2	AAW31273	Mouse tri
411	34	60.7	572	8	ADO29338	Mouse GPC
412	34	60.7	572	9	ADZ13020	Murine ca
413	34	60.7	574	6	ABU55902	Human pro
414	34	60.7	574	7	Aae33056	FZD7 prot
415	34	60.7	574	7	ADG74269	Human fri
416	34	60.7	574	8	ADN03982	Antipiori
417	34	60.7	574	8	ADO29337	Human GPC
418	34	60.7	574	8	ADQ2264	Human FZD
419	34	60.7	574	8	ADQ18461	Human sof
420	34	60.7	574	8	ADS92964	Frizziel
421	34	60.7	574	8	ADU06307	Novel bro
422	34	60.7	574	9	ADU13023	Human can
423	34	60.7	574	9	ABP28131	Human Fri
424	34	60.7	595	4	ABB60297	Drosophil
425	34	60.7	610	4	ABG06352	Novel hum
426	34	60.7	629	7	ADH54846	Human ins
427	34	60.7	666	4	ABB11769	Human dJ3
428	34	60.7	666	4	ADM79751	Human pro
429	34	60.7	693	7	ADM85550	Mouse pro
430	34	60.7	764	5	ABB05596	Human tes
431	34	60.7	769	8	ABO59732	Human Gen
432	34	60.7	814	8	ADH22503	Human tra
433	34	60.7	829	8	ADS99456	Human kin
434	34	60.7	830	8	ADY97905	Murine pr
435	34	60.7	842	4	ADM93906	Murine ki
436	34	60.7	842	8	ADL32020	Human pro
437	34	60.7	945	4	Aau03538	Human Pro
438	34	60.7	945	5	AEE19157	Human kin
439	34	60.7	965	9	ADV97905	Murine pr
440	34	60.7	971	7	ADU3116	Human apo
441	34	60.7	976	5	ABP35659	Fungal ZB
442	34	60.7	982	8	ADJ96663	Human tyr
443	34	60.7	1000	6	ADU8810	Human Gli
444	34	60.7	1127	4	ABC22813	Novel hum
445	34	60.7	1147	8	ADH22510	Human tra
446	34	60.7	1163	7	ADM29272	Human nov
447	34	60.7	1239	6	ADM29274	Human NOV
448	34	60.7	1239	6	Aau91183	Human HEA
449	34	60.7	1280	7	ABR62331	Human cat
450	34	60.7	1280	7	ADk18348	Human NOV
451	34	60.7	1280	7	ADM29272	Human nov
452	34	60.7	1280	8	ADT79949	Human O
453	34	60.7	1280	8	ABU48705	Protein e
454	34	60.7	1596	5	Aao17114	Human Gli
455	34	60.7	1596	8	ADQ17743	Human sof
456	34	60.7	1597	9	AEQ27510	Human zin
457	34	60.7	1597	9	Aea30113	Glioblast
458	34	60.7	1774	8	ADR10354	Human pro
459	34	60.7	1862	8	ADl39685	Streptomy
460	34	60.7	1995	8	ADl26784	Human Shr
461	34	60.7	3913	6	ABM67350	Photorhab
462	34	59.8	741	8	ADS42907	Bacterial

23	2	58.9	33	33	AAW66468	Cationic
23	3	58.9	23	33	AAy91167	Cationic
23	3	58.9	23	33	ABU59445	Tumor cel
23	9	58.9	23	33	ADY67516	Propionib
23	9	58.9	54	33	Aau39503	Propionib
23	9	58.9	54	33	ABM36122	Enterococ
23	7	58.9	60	33	ADH86709	Bacterial
23	7	58.9	61	33	ADP04788	Yeast smo
23	7	58.9	65	33	Ada33468	Actinobac
23	7	58.9	65	33	Ada57293	Human sec
23	7	58.9	67	33	Abm61900	Propionib
23	7	58.9	67	33	Ada41173	Human sec
23	7	58.9	67	33	Aag74375	Human sec
23	7	58.9	69	33	Adf04113	Bacterial
23	7	58.9	75	33	Adh32461	Plant ful
23	7	58.9	75	33	Adm91027	Human imm
23	7	58.9	78	33	AAW65381	Propionib
23	7	58.9	79	33	Abm61900	Propionib
23	7	58.9	82	33	Aab54363	Human col
23	7	58.9	82	33	Abg74079	Human col
23	7	58.9	85	33	Ady11334	Plant ful
23	7	58.9	97	33	ABP07985	Human ORF
23	7	58.9	99	33	ABR56776	Human sec
23	7	58.9	101	33	AAU58381	Propionib
23	7	58.9	101	33	Abm54900	Propionib
23	7	58.9	101	33	Adr09722	Novel hum
23	7	58.9	105	33	Aab42868	Human ORF
23	7	58.9	105	33	Adm92222	Human dig
23	7	58.9	116	33	Abb16132	Human ner
23	7	58.9	122	33	Aam9458	Human pro
23	7	58.9	123	33	AAU86426	Human pro
23	7	58.9	123	33	Adw80359	Human pro
23	7	58.9	128	33	ABG02051	Novel hum
23	7	58.9	128	33	Adx76105	Plant ful
23	7	58.9	131	33	ABo57453	Human gen
23	7	58.9	131	33	Adm25800	Hyperther
23	7	58.9	131	33	Aau63378	Propionib
23	7	58.9	131	33	ABG02049	Novel hum
23	7	58.9	131	33	Aar13016	Deaceyl
23	7	58.9	131	33	Aae03257	Human gen
23	7	58.9	131	33	Ady22154	Rat immun
23	7	58.9	131	33	Aab93502	Human pro
23	7	58.9	131	33	Aae03223	Human gen
23	7	58.9	131	33	Abu13083	Human alb
23	7	58.9	131	33	ABG64391	Human ORF
23	7	58.9	131	33	Abp64543	Human ORF
23	7	58.9	131	33	Adl77558	Albumin f
23	7	58.9	131	33	Aee03256	Human gen
23	7	58.9	131	33	Aab55114	Pseudomon
23	7	58.9	131	33	Aab5512	Pseudomon
23	7	58.9	131	33	Abj19779	Human MP2
23	7	58.9	202	33	ABU19795	Deatch as
23	7	58.9	202	33	Abu38104	Protein e
23	7	58.9	202	33	Abu09417	Novel hum
23	7	58.9	202	33	Abos5922	Pseudomon
23	7	58.9	202	33	Adr51331	Anti-biof
23	7	58.9	202	33	Aab98360	Cat SCF p
23	7	58.9	202	33	Aab02486	Cat SCF l
23	7	58.9	202	33	Aab5921	Cat SCF -
23	7	58.9	202	33	Aab02772	Cat SCF -
23	7	58.9	202	33	Aau02772	Cat stem
23	7	58.9	202	33	Ade05259	Cat stem
23	7	58.9	202	33	Adz52480	Cat stem
23	7	58.9	271	33	Adp99322	Cat stem
23	7	58.9	271	33	Adu05052	Cat stem
23	7	58.9	271	33	Adw93397	Cat stem
23	7	58.9	271	33	Adz47549	Cat stem

536	273	7	ABO68701	Pseudomon	Nov	
537	33	274	AAN0979	Feline st	Nov	
538	33	274	AAB56945	Cat stem	Gen	
539	33	274	AD247607	Cat stem	Human bon	
540	33	274	ADX90889	Plant ful	Human pol	
541	33	287	8	ABP28320	Anino aci	Human pro
542	33	296	6	ABU92057	Human pro	Add18995
543	33	296	6	ADY11741	Plant ful	Human dis
544	33	303	9	ADQ65470	Novel hum	Adw42864
545	33	303	8	ADX65974	Plant ful	Adw42857
546	33	303	8	ADB74340	Mycobacte	Human met
553	33	320	8	ADP25089	PRO polyp	Abg25104
554	33	324	7	ADP51716	St-reptomy	Pinus rad
548	33	329	8	ADP51716	St-reptomy	Abm87868
549	33	329	8	ABP41389	Human ova	Rice abio
550	33	334	5	ADL77660	Albumin f	Adn20558
556	33	334	6	ADA34527	Actinetobac	Bacterial
551	33	334	6	ABD68392	Drosophil	Abn75508
552	33	334	7	ABP43860	MGC : 1127	Protein O
558	33	349	5	AAB03206	Human gen	Ado77904
559	33	349	5	AAB64393	Human alb	Ado25104
560	33	359	5	AAB79772	Novel hum	ABR8768
561	33	359	8	ABO59722	Human gen	Ado87868
562	33	359	8	ADL77660	Human ful	Ado25104
563	33	368	2	AAV41496	Fragment	Ado18995
557	33	368	3	AAB75212	Drosophil	Ado10398
558	33	379	4	AAB68392	Drosophil	Ado10398
559	33	379	4	AAB30514	Fruit fly	Ado10398
565	33	379	5	ADM26461	Flyerther	Ado10398
566	33	379	5	AAB29772	Novel hum	Ado10398
567	33	379	8	ABO59722	Human alb	Ado10398
568	33	379	8	ADL77660	Human ful	Ado10398
569	33	379	4	AAB42293	Cephaloop	Ado10398
570	33	379	4	ABG12792	Drosophil	Ado10398
571	33	379	5	ADM26461	Novel hum	Ado10398
572	33	379	5	AAB70072	Human sec	Ado10398
573	33	379	5	AAB65511	Human alb	Ado10398
574	33	379	8	ADL77660	Human ful	Ado10398
575	33	379	4	AAB42293	Human hyp	Ado10398
576	33	379	4	ABG2097	Novel hum	Ado10398
577	33	379	5	AAR35072	Human pro	Ado10398
578	33	379	5	AAB50231	Human tra	Ado10398
579	33	379	5	ADR14239	Human nuc	Ado10398
580	33	379	8	ADL77660	Human NF-	Ado10398
581	33	379	8	ADT78778	Human ful	Ado10398
582	33	379	8	ADP56783	Drosophil	Ado10398
583	33	379	8	ABG12792	Drosophil	Ado10398
584	33	379	8	ABP50231	Novel hum	Ado10398
585	33	379	8	ADR14239	Propionib	Ado10398
586	33	379	8	ADT78778	Propionib	Ado10398
587	33	379	8	ADP56783	Propionib	Ado10398
588	33	379	8	ABG2097	Propionib	Ado10398
589	33	379	8	AAR35072	Propionib	Ado10398
590	33	379	8	AAB50231	Propionib	Ado10398
591	33	379	8	ADR14239	Propionib	Ado10398
592	33	379	8	ADL77660	Propionib	Ado10398
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725	32	57.1	ADM05223	Human pro	798	32	
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747	32	57.1	ADQ67105	Novel hum	819	32	
748	32	57.1	AAG28363	Arabidops	820	32	
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763	32	57.1	ABO60268	Human gen	764	32	
764	32	57.1	AAM16081	Peptid#	765	32	
765	32	57.1	Abb35070	Peptid#	766	32	
766	32	57.1	Abb29890	Peptid#	767	32	
767	32	57.1	Abb20486	Protein#	768	32	
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769	32	57.1	Adl05960	M. catarr	770	32	
770	32	57.1	ABP03885	Human ORF	771	32	
771	32	57.1	Abg49912	Human liv	772	32	
772	32	57.1	Aam03808	Peptid#	773	32	
773	32	57.1	Abg37793	Human pep	774	32	
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775	32	57.1	Abp06560	M. catarr	776	32	
776	32	57.1	Abp0802	Propionib	777	32	
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778	32	57.1	Abg19625	Human hum	779	32	
779	32	57.1	Ady64460	Human APO	780	32	
780	32	57.1	Aam87554	Human imm	781	32	
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782	32	57.1	Aay36379	Fragment	783	32	
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792	32	57.1	Aab94945	Human pro	793	32	
793	32	57.1	Abm6488	M. xanthi	794	32	
794	32	57.1	Aar11793	Histo-blo	795	32	
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796	32	57.1	Aar57017	Human O t	797	32	
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809	32	57.1	ADM1003	Human nov	810	32	
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811	32	57.1	AAB64117	Human pro	812	32	
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813	32	57.1	AAG48139	Arabidops	814	32	
814	32	57.1	AAB63137	Arabidops	815	32	
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818	32	57.1	Abm64805	Human pro	819	32	
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842	32	57.1	ADJ54634	Human APO	843	32	
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845	32	57.1	Abm91359	Human APO	846	32	
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847	32	57.1	Abm64313	Bacterial	848	32	
848	32	57.1	Abm21689	Bacterial	849	32	
849	32	57.1	ADn24444	Bacterial	850	32	

828	57.1	310	8	ADN26091	Bacterial	Ada95618	Human	PRO
829	57.1	312	8	ADT08349	Plant ful	Adb25927	Human	PRO
830	57.1	315	4	AAU58257	Propionib	Adb21412	Novel	hum
831	57.1	32	57.1	ABM54776	Propionib	Ada77191	Human	PRO
832	57.1	32	57.1	ADK94660	Plant ful	Adb17931	7	ADA77191
833	57.1	32	57.1	AAB7744	Human T2R	Ada86614	Novel	hum
834	57.1	32	57.1	ADU84507	Human T2R	Ada87717	Novel	hum
835	57.1	32	57.1	ADR29087	Taste rec	ADA46105	Novel	hum
836	57.1	32	57.1	ADM33327	Human bit	Ada09126	Novel	hum
837	57.1	32	57.1	ADX91925	Plant ful	Adb28135	Human	PRO
838	57.1	32	57.1	ADW74528	Human bit	Adb28687	Human	PRO
839	57.1	32	57.1	ADW74530	Human bit	Ada76639	Human	PRO
840	57.1	32	57.1	ADW74408	Human bit	Ada88269	Novel	hum
841	57.1	32	57.1	ADW74526	Human bit	Ada97274	Human	PRO
842	57.1	32	57.1	ADA54228	Human pro	Adb27031	Human	PRO
843	57.1	32	57.1	ABR88041	Human GI	Adb21964	Novel	hum
844	57.1	32	57.1	AAU57697	Propionib	Ada66555	Human	PRO
845	57.1	32	57.1	ABM64216	Propionib	Adb22516	Human	PRO
846	57.1	32	57.1	ADU02616	Novel hum	Adb23289	Human	PRO
847	57.1	32	57.1	ADU02616	Novel ful	Ada92011	Novel	hum
848	57.1	32	57.1	AAB94848	Human pro	Adb15074	Human	PRO
849	57.1	32	57.1	AAB27777	Human ful	Adb38326	Novel	hum
850	57.1	32	57.1	AAU2188	Human ful	Adb37774	Novel	hum
851	57.1	32	57.1	ABU6589	Human bit	Adb66246	Novel	hum
852	57.1	32	57.1	ABU6589	Human amy	Adb66246	Novel	hum
853	57.1	32	57.1	ABU08213	Human car	Adb89326	Human	PRO
854	57.1	32	57.1	ADX77816	Plant ful	Adb90058	Human	PRO
855	57.1	32	57.1	AAB94816	Human lya	Adb39159	Novel	hum
856	57.1	32	57.1	AAB017632	Human pro	Adb46792	Novel	hum
857	57.1	32	57.1	AABU0886	Human PRO	Adb86389	Human	PRO
858	57.1	32	57.1	ABU65896	Human PRO	Adb76934	Novel	hum
859	57.1	32	57.1	ABU65896	Human sec	Adb34151	Human	PRO
860	57.1	32	57.1	ABU08902	Human sec	Adb35255	Human	PRO
861	57.1	32	57.1	ABU08902	Human sec	Adb33559	Human	PRO
862	57.1	32	57.1	ABU65896	Human sec	Adb34703	Human	PRO
863	57.1	32	57.1	ABU65896	Human sec	Adb35807	Human	PRO
864	57.1	32	57.1	ABU65896	Human sec	Adb46202	Novel	hum
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866	57.1	32	57.1	ADA45553	Novel hum	Adb71622	Novel	hum
867	57.1	32	57.1	ADA75984	Human PRO	Adc59601	Novel	hum
868	57.1	32	57.1	ADA18634	Human PRO	Adb52608	Novel	hum
869	57.1	32	57.1	ADA61257	Human sap1	Adc59692	Novel	hum
870	57.1	32	57.1	ADB19042	Novel hum	Adc60153	Novel	hum
871	57.1	32	57.1	ADB27583	Human PRO	Adc50628	Novel	hum
872	57.1	32	57.1	ADA86052	Novel hum	Adc565155	Human	PRO
873	57.1	32	57.1	ADA15626	Human PRO	Adc54253	Novel	hum
874	57.1	32	57.1	ADA47412	Human PRO	Adc53214	Novel	hum
875	57.1	32	57.1	ADA67207	Human PRO	Adc58737	Novel	hum
876	57.1	32	57.1	ADB30214	Human PRO	Adc55615	Novel	hum
877	57.1	32	57.1	ADA91459	Novel hum	Adc58185	Novel	hum
878	57.1	32	57.1	ADA95510	Novel hum	Adc02859	Novel	hum
879	57.1	32	57.1	ADA96722	Human PRO	Adc80219	Novel	hum
880	57.1	32	57.1	ADA79026	Human PRO	Adc10726	Human	PRO
881	57.1	32	57.1	ADA47480	Novel hum	Adc79667	Novel	hum
882	57.1	32	57.1	ADA12906	Human PRO	Ada09136	Human	PRO
883	57.1	32	57.1	ABO43165	Novel hum	Ada04263	Novel	hum
884	57.1	32	57.1	ADA74160	Human PRO	Ada51988	Novel	hum
885	57.1	32	57.1	ADA95433	Human PRO	Ada52278	Human	PRO
886	57.1	32	57.1	ADA93698	Human PRO	Ada47607	Human	PRO
887	57.1	32	57.1	ADA87165	Novel hum	Ada53280	Novel	hum
888	57.1	32	57.1	ADA16367	Human PRO	Ada48159	Human	PRO
889	57.1	32	57.1	ADA91459	Novel hum	Ada09688	Human	PRO
890	57.1	32	57.1	ADA95510	Novel hum	Ada040849	Novel	hum
891	57.1	32	57.1	ADA81917	Human PRO	Ada52278	Human	PRO
892	57.1	32	57.1	ADA19594	Novel hum	Ada51436	Human	PRO
893	57.1	32	57.1	ADA84958	Novel hum	Ada02235	Human	PRO
894	57.1	32	57.1	ADA84406	Novel hum	Ada01659	Human	PRO
895	57.1	32	57.1	ADA29662	Human PRO	Ada53851	Novel	hum
896	57.1	32	57.1	ADA80190	Human PRO	Ada92168	Novel	hum
897	57.1	32	57.1	ADA80766	Human PRO	Ada0694	Human	PRO
898	57.1	32	57.1	ADA80766	Human PRO	Ada03678	Human	PRO
899	57.1	32	57.1	ADA823841	Human PRO	Ada31975	Novel	hum
900	57.1	32	57.1	ADA80742	Human PRO	Ada21907	Human	PRO

974 32 57.1 328 7 ADD79131 Human PRO  
975 32 57.1 328 7 ADB41667 Human PRO  
976 32 57.1 328 7 Ade17484 Human PRO  
977 32 57.1 328 7 ADD91616 Human PRO  
978 32 57.1 328 7 Ade33079 Novel hum  
979 32 57.1 328 7 Ade33631 Novel hum  
980 32 57.1 328 7 ADD79683 Human PRO  
981 32 57.1 328 7 ADD92720 Human PRO  
982 32 57.1 328 7 Ade19140 Human PRO  
983 32 57.1 328 7 ADB18588 Human PRO  
984 32 57.1 328 7 Ade42784 Human PRO  
985 32 57.1 328 7 ADD95573 Human PRO  
986 32 57.1 328 7 Ade22459 Human PRO  
987 32 57.1 328 7 ADD78577 Human PRO  
988 32 57.1 328 7 Ade32527 Novel hum  
989 32 57.1 328 7 Ade42219 Human PRO  
990 32 57.1 328 7 Add80235 Human PRO  
991 32 57.1 328 7 Ade40547 Human PRO  
992 32 57.1 328 7 Ade04346 Human PRO  
993 32 57.1 328 7 Ade92475 Human PRO  
994 32 57.1 328 7 ADG21184 Novel hum  
995 32 57.1 328 7 ADG22825 Novel hum  
996 32 57.1 328 7 Ade97160 Human PRO  
997 32 57.1 328 7 Adg80224 Human PRO  
998 32 57.1 328 7 Ade79672 Human PRO  
999 32 57.1 328 7 Ade54964 Novel hum  
1000 32 57.1 328 7 ADH54964 Novel hum

## ALIGNMENTS

RESULT 1  
ADD115844  
ID ADD115844 standard; peptide; 10 AA.

XX AC;  
XX DT 22-APR-2004 (first entry)

XX DE HLA-A2 restricted cytotoxic T lymphocyte recognised peptide #187.  
XX tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;  
XX cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;  
XX stomach cancer; buccal cancer; renal cancer; lung cancer;  
XX gynaecological cancer; prostate cancer.  
XX Synthetic.  
XX PN WO2003008450-A1.  
XX PD 30-JAN-2003.  
XX PF 11-JUN-2002; 2002WO-JP005799.  
XX PR 12-JUN-2001; 2001JP-00177058.  
XX PR 21-AUG-2001; 2001JP-00250728.  
XX PA (Itoh K.) ITOH K.  
XX PI Itoh K., Shichijo S.;  
XX DR WPI; 2003-267996/26.  
XX Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or  
PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of  
PT cancer including preparation of cancer vaccines.

XX Claim 1; SEQ ID NO 188; 323PP; Japanese.

XX The invention relates to a tumour antigen peptide recognised by human  
CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL). The tumour antigen peptide is useful for  
CC and/or capable of inducing CTL. The tumour antigen peptide is useful for  
CC the treatment, prevention, diagnosis and vaccine production for cancers  
CC including colorectal, stomach, buccal, renal, lung, gynaecological and  
CC HLA-A2 restricted cytotoxic T lymphocytes.  
XX SQ Sequence 10 AA;

Query Match	100.0%	Score 56;	DB 7;	Length 10;
Best Local Similarity	100.0%;	Pre. NO. 0.022;	0;	
Matches	10;	Conservative	0;	Gaps 0;
Qy	1 LMALPPCHAL 10			
Db	1 LMALPPCHAL 10			

RESULT 2  
ABG20769  
ID ABG20769 standard; protein; 216 AA.

AC	ABG20769;			
XX	XX	18-FEB-2002 (first entry)	DT	18-FEB-2002 (first entry)
XX	XX	Novel human diagnostic protein #20760.	DE	Novel human diagnostic protein #20760.
XX	XX	Human; chromosome mapping; gene mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.	KW	Human; chromosome mapping; gene mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
XX	XX	Homo sapiens.	OS	Homo sapiens.
XX	XX	WO200175067-A2.	PN	WO200175067-A2.
XX	XX	11-OCT-2001.	PD	11-OCT-2001.
XX	XX	30-MAR-2001; 2001WO-US008631.	PP	30-MAR-2001; 2001WO-US008631.
XX	XX	31-MAR-2000; 2000US-00540217.	PR	31-MAR-2000; 2000US-00540217.
XX	XX	23-AUG-2000; 2000US-00659167.	PR	23-AUG-2000; 2000US-00659167.
XX	XX	(HYSE-) HYSEQ INC.	XX	(HYSE-) HYSEQ INC.
XX	XX	Dramanac RT, Liu C, Tang YT;	PI	Dramanac RT, Liu C, Tang YT;
XX	XX	DR WPI; 2001-639362/73.	DR	DR WPI; 2001-639362/73.
XX	XX	DR N-PSDB; AS84936.	DR	DR N-PSDB; AS84936.
XX	XX	New isolated polynucleotide and encoded polypeptides, useful in PT diagnostics, forensics, gene mapping, identification of mutations PT responsible for genetic disorders or other traits and to assess PT biodiversity.	PT	New isolated polynucleotide and encoded polypeptides, useful in PT diagnostics, forensics, gene mapping, identification of mutations PT responsible for genetic disorders or other traits and to assess PT biodiversity.
XX	XX	Claim 20; SEQ ID NO 51128; 103PP; English.	PS	Claim 20; SEQ ID NO 51128; 103PP; English.
XX	XX	The invention relates to isolated polynucleotide (I) and polypeptide (II) CC sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for generic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG0010-ABG30377 represents novel human diagnostic CC amino acid sequences. The invention Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in	CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) CC sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for generic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG0010-ABG30377 represents novel human diagnostic CC amino acid sequences. The invention Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at  
 CC [ftp.wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 216 AA;

Query Match	100.0%	Score 56;	DB 4;	Length 216;
Best Local Similarity	100.0%	Pred. No.	0.39;	
Matches	10;	Mismatches	0;	Indels 0;
Gaps	0;			

Qy 1 LMALPPCHAL 10  
 Db 116 LMALPPCHAL 125

XX RESULT 3  
 ADC56779 standard; protein, 230 AA.  
 XX ID ADC56779;  
 XX AC ADC56779;  
 XX DT 18-DEC-2003 (first entry)  
 XX DS Splice variant 1 of human thymidylic acid synthetase protein.  
 XX KW human; thymidylic acid synthetase; hTS; cancer; anticancer; EC 2.1.1.45.  
 XX OS Homo sapiens.  
 XX PN JP2003102480-A.  
 XX PD 08-APR-2003.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX WPI; 2003-649087/62.  
 XX DR N-PSDB; ADC56768.  
 XX Disclosure; Page 22-23; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 2003-649087/62.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56767.  
 XX Disclosure; Page 20-21; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56767.  
 XX Disclosure; Page 20-21; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56768.

XX RESULT 4  
 ADC56780 standard; protein, 279 AA.  
 XX ID ADC56780;  
 XX AC ADC56780;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Splice variant 2 of human thymidylic acid synthetase protein.  
 XX KW human; thymidylic acid synthetase; hTS; cancer; anticancer; EC 2.1.1.45.  
 XX OS Homo sapiens.  
 XX PN JP2003102480-A.  
 XX PD 08-APR-2003.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56768.  
 XX Disclosure; Page 22-23; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 2003-649087/62.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56767.  
 XX Disclosure; Page 20-21; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56767.  
 XX Disclosure; Page 20-21; 28pp; Japanese.  
 XX PN JP2003102480-A.  
 XX PR 28-SEP-2001; 2001JP-00300086.  
 XX PA (SRLS-) SRL KK.  
 XX DR N-PSDB; ADC56768.

XX RESULT 5  
 ABP53743 standard; protein, 284 AA.  
 XX ID ABP53743;  
 XX AC ABP53743;  
 XX DT 02-JAN-2003 (first entry)  
 XX SQ Sequence 230 AA;  

Query Match	100.0%	Score 56;	DB 7;	Length 230;
Best Local Similarity	100.0%	Pred. No.	0.41;	
Matches	10;	Mismatches	0;	Indels 0;
Gaps	0;			

Qy 1 LMALPPCHAL 10  
 Db 106 LMALPPCHAL 115

XX Human thymidylate synthase amino acid sequence.

KW Thymidylate synthase; enzyme; binding; neoplastic disorder;  
 KW chemotherapeutic; cytostatic; thymidylate synthase inhibitor; cancer.

XX OS Homo sapiens.

XX Key Location/Qualifiers  
 31..47 /label= Peptide<sup>9</sup>  
 /note= "thymidylate synthase binding peptide"

FT PT Peptide 56..72 /label= Peptide<sup>14</sup>  
 /note= "thymidylate synthase binding peptide"

FT PT Peptide 131..147 /label= Peptide<sup>29</sup>  
 /note= "thymidylate synthase binding peptide"

FT PT Peptide 175..192 /label= Peptide<sup>38</sup>  
 /note= "thymidylate synthase binding peptide"

FT PT Peptide 201..217 /label= Peptide<sup>43</sup>  
 /note= "thymidylate synthase binding peptide"

XX PN WO200272753-A2.  
 XX PD 19-SEP-2002.  
 XX PP 05-MAR-2002; 2002WO-US006634.  
 XX PR 07-MAR-2001; 2001US-0274107P.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Allegra CJ, Vobeller DM;  
 XX DR 2002-732823/79.  
 WPI; 2002-732823/79.

PT New isolated peptide binding to an mRNA encoding thymidylate synthase - used to, e.g. develop products useful for treating and/or diagnosing disorders such as cancer of a head and neck, breast, prostate, liver, lung, gastric, colon or esophagus.

XX PS Example 2; Fig 1B; 59pp; English.

XX The present invention describes a peptide (1) which binds to an mRNA encoding a thymidylate synthase (TS) polypeptide. Also described: (1) inhibiting translation of a mRNA encoding TS comprising contacting the mRNA, or a cell expressing the mRNA with a peptide comprising 10-25 consecutive amino acids of the peptide interface region of the TS, where the peptide binds to the mRNA encoding TS, and inhibits the translation of the mRNA encoding TS; and (2) treating a subject with a neoplastic disorder comprising administering to the subject a chemotherapeutic agent and a TS peptide or a therapeutic nucleic acid sequence comprising a promoter operably linked to a nucleic acid sequence encoding TS peptide that comprises 10-25 amino acids of the peptide interface region of the TS, where the peptide binds to the mRNA encoding TS, and inhibits the translation of the mRNA encoding TS, treating the neoplastic disorder. (1) has cytostatic activity, and can be used as a TS inhibitor. The methods and compositions of the present invention are useful for treating and/or diagnosing disorders associated with the TS peptide, such as cancer of a head and neck, breast, prostate, liver, lung, gastric, colon or esophagus. They are also used to enhance the effect of other chemotherapeutic agents. The present sequence represents a human thymidylate synthase amino acid sequence, which is used in an example from the present invention

XX SQ Sequence 284 AA;

CC The present invention describes a peptide (1) which binds to an mRNA encoding a thymidylate synthase (TS) polypeptide. Also described: (1) inhibiting translation of a mRNA encoding TS comprising contacting the mRNA, or a cell expressing the mRNA with a peptide comprising 10-25 consecutive amino acids of the peptide interface region of the TS, where the peptide binds to the mRNA encoding TS, and inhibits the translation of the mRNA encoding TS; and (2) treating a subject with a neoplastic disorder comprising administering to the subject a chemotherapeutic agent and a TS peptide or a therapeutic nucleic acid sequence comprising a promoter operably linked to a nucleic acid sequence encoding TS peptide that comprises 10-25 amino acids of the peptide interface region of the TS, where the peptide binds to the mRNA encoding TS, and inhibits the translation of the mRNA encoding TS, treating the neoplastic disorder. (1) has cytostatic activity, and can be used as a TS inhibitor. The methods and compositions of the present invention are useful for treating and/or diagnosing disorders associated with the TS peptide, such as cancer of a head and neck, breast, prostate, liver, lung, gastric, colon or esophagus. They are also used to enhance the effect of other chemotherapeutic agents. The present sequence represents a human thymidylate synthase amino acid sequence, which is used in an example from the present invention

XX SQ Sequence 313 AA;

CC Sequences AAW5752-W75768 represent thymidylate synthase (TS) mutants most of which were generated by using site directed mutagenesis. This was performed by creating a TS expression vector pCDNA3hTS which contained the human TS gene coding sequence, and using this to produce ssDNA for site-directed mutagenesis and sequence analysis. Mutants which were not produced this way were produced by random mutagenesis, by exposing human sarcoma HT1080 cells to an alkylating agent and then using AG337 for selection. From these mutagenesis experiments 17 different mutants were obtained, each of which were mutated at one of five different amino acid positions causing an amino acid change and thus causing the TS enzyme to have different properties. It was found that mutations at positions 49 and 52 caused the enzyme to form resistance to AG337 and FuDrd, whereas mutations at 108 were found to confer tamox and AG337 resistance. In general mutated TS cDNAs have been found to be resistant to TS specificity inhibitors, and to have a high catalytic efficiency and good stability. The mutant TS cDNA can be used in gene therapy to transfer drug resistance to human haematopoietic progenitors, thus allowing dose-intense therapy in cancer patients by protecting normal cells and preventing dose-limiting myelotoxicity. N.B. The present sequence is not shown in the specification but was derived from the TS wild-type sequence, also not given in the specification

XX SQ Sequence 313 AA;

CC Sequences 100..0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100..0%; Pred. No. 0..5%;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

CC Query Match 100..0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100..0%; Pred. No. 0..5%;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 9  
 AAW75757  
 ID AAW75757 standard; protein; 313 AA.  
 XX  
 AC AAW75757;  
 XX DT 19-NOV-1998 (first entry)  
 DB Mutated thymidylate synthase.  
 XX  
 KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 KW tumudex; gene therapy; cancer; myelotoxicity.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FH Misc-difference 108 /note= "Wild-type Ile substituted by Gly"  
 FT PT XX WO9833518-A1.  
 PN PD XX 06-AUG-1998.  
 XX PP 03-FEB-1998; 98WO-US002145.  
 PR XX 04-FEB-1997; 97US-0037163P.  
 XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 DR XX WPI; 1998-437173/37.  
 XX  
 PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 XX  
 PS Claim 4; Page: 78pp; English.  
 XX  
 Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 most of which were generated by using site directed mutagenesis. This was  
 performed by creating a TS expression vector pCDNA3hts which contained  
 the human TS gene coding sequence, and using this to produce ssDNA for  
 site-directed mutagenesis and sequence analysis. Mutants which were not  
 created this way were produced by random mutagenesis, by exposing human  
 sarcoma HT100 cells to an alkylating agent and then using AG337 for  
 selection. From these mutagenesis experiments, 17 different mutants were  
 obtained, each of which were mutated at one of five different amino acid  
 positions causing an amino acid change and thus causing the TS enzyme to  
 have different properties. It was found that mutations at positions 49  
 and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 mutations at 108 were found to confer tumudex and AG337 resistance. In  
 general mutated TS cDNAs have been found to be resistant to TS specific  
 inhibitors, and to have a high catalytic efficiency and good stability.  
 The mutant TS cDNA can be used in gene therapy to transfer drug  
 resistance to human haematopoietic progenitors, thus allowing dose-  
 intensive therapy in cancer patients by protecting normal cells and  
 preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 shown in the specification but was derived from the TS wild-type  
 sequence, also not given in the specification  
 XX Sequence 313 AA;

RESULT 10  
 AAW75766  
 ID AAW75766 standard; protein; 313 AA.  
 XX  
 AC AAW75766;  
 XX DT 19-NOV-1998 (first entry)  
 DE Mutated thymidylate synthase.  
 XX  
 KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 KW tumudex; gene therapy; cancer; myelotoxicity.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FH Misc-difference 225 /note= "Wild-type Phe substituted by Ser"  
 FT PT XX WO9833518-A1.  
 PN PD XX 06-AUG-1998.  
 XX PP 03-FEBB-1998; 98WO-US002145.  
 PR XX 04-FEBB-1997; 97US-0037163P.  
 XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 DR XX WPI; 1998-437173/37.  
 XX  
 PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 XX  
 PS Claim 6; Page: 78pp; English.  
 XX  
 Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 most of which were generated by using site directed mutagenesis. This was  
 performed by creating a TS expression vector pCDNA3hts which contained  
 the human TS gene coding sequence, and using this to produce ssDNA for  
 site-directed mutagenesis and sequence analysis. Mutants which were not  
 created this way were produced by random mutagenesis, by exposing human  
 sarcoma HT100 cells to an alkylating agent and then using AG337 for  
 selection. From these mutagenesis experiments, 17 different mutants were  
 obtained, each of which were mutated at one of five different amino acid  
 positions causing an amino acid change and thus causing the TS enzyme to  
 have different properties. It was found that mutations at positions 49  
 and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 mutations at 108 were found to confer tumudex and AG337 resistance. In  
 general mutated TS cDNAs have been found to be resistant to TS specific  
 inhibitors, and to have a high catalytic efficiency and good stability.  
 The mutant TS cDNA can be used in gene therapy to transfer drug  
 resistance to human haematopoietic progenitors, thus allowing dose-  
 intensive therapy in cancer patients by protecting normal cells and  
 preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 shown in the specification but was derived from the TS wild-type  
 sequence, also not given in the specification  
 XX Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

**RESULT 11**

AAW75752  
ID AAW75752 standard; protein; 313 AA.  
XX  
AC AAW75752;  
XX DT 19-NOV-1998 (first entry)  
XX DB Mutated thymidylate synthase.  
XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Fdurd;  
KW tumudex; gene therapy; cancer; myelotoxicity.  
XX OS Homo sapiens.  
OS Synthetica.  
XX FH Key  
FT Misc-difference 49 Location/Qualifiers  
/note= "Wild-type Asp substituted by Asn"  
XX PN WO9833518-A1.  
XX PD 06-AUG-1998.  
XX PP 03-FEB-1998; 98WO-US002145.  
XX PR 04-FEB-1997; 97US-0037163P.  
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
XX DR 1998-437173/37.  
XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
PT for use in gene therapy and for treating cancers.  
XX PS Claim 2; Page: 78pp; English.  
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
CC most of which were generated by using site directed mutagenesis. This was  
CC performed by creating a TS expression vector pcDNA3hts which contained  
the human TS gene coding sequence, and using this to produce ssDNA for  
site-directed mutagenesis and sequence analysis. Mutants which were not  
created this way were produced by random mutagenesis, by exposing human  
sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
selection. From these mutagenesis experiments, 17 different mutants were  
obtained, each of which were mutated at one of five different amino acid  
positions causing an amino acid change and thus causing the TS enzyme to  
have different properties. It was found that mutations at positions 49  
and 52 caused the enzyme to form resistance to AG337 and Fdurd, whereas  
mutations at 108 were found to confer tumudex and AG337 resistance. In  
general, mutated TS cDNAs have been found to be resistant to TS specific  
inhibitors, and to have a high catalytic efficiency and good stability.  
The mutant TS cDNA can be used in gene therapy to transfer drug  
resistance to human haematopoietic progenitors, thus allowing dose-  
intense therapy in cancer patients by protecting normal cells and  
preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
shown in the specification but was derived from the TS wild-type  
sequence, also not given in the specification  
XX Sequence 313 AA;  
SQ Score 56; DB 2; Length 313;  
Query Match 100.0%; Score 56; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 12**

AAW75763  
ID AAW75763 standard; protein; 313 AA.  
XX  
AC AAW75763;  
XX DT 19-NOV-1998 (first entry)  
XX DE Mutated thymidylate synthase.  
XX KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Fdurd;  
KW tumudex; gene therapy; cancer; myelotoxicity.  
XX OS Homo sapiens.  
OS Synthetica.  
XX FH Key  
FT Misc-difference 221 Location/Qualifiers  
/note= "Wild-type Leu substituted by Ile"  
XX PN WO9833518-A1.  
XX PD 06-AUG-1998.  
XX PP 03-FEB-1998; 98WO-US002145.  
XX PR 04-FEB-1997; 97US-0037163P.  
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
XX DR 1998-437173/37.  
XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
PT for use in gene therapy and for treating cancers.  
XX PS Claim 5; Page: 78pp; English.  
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
CC most of which were generated by using site directed mutagenesis. This was  
CC performed by creating a TS expression vector pcDNA3hts which contained  
the human TS gene coding sequence, and using this to produce ssDNA for  
site-directed mutagenesis and sequence analysis. Mutants which were not  
created this way were produced by random mutagenesis, by exposing human  
sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
selection. From these mutagenesis experiments, 17 different mutants were  
obtained, each of which were mutated at one of five different amino acid  
positions causing an amino acid change and thus causing the TS enzyme to  
have different properties. It was found that mutations at positions 49  
and 52 caused the enzyme to form resistance to AG337 and Fdurd, whereas  
mutations at 108 were found to confer tumudex and AG337 resistance. In  
general, mutated TS cDNAs have been found to be resistant to TS specific  
inhibitors, and to have a high catalytic efficiency and good stability.  
The mutant TS cDNA can be used in gene therapy to transfer drug  
resistance to human haematopoietic progenitors, thus allowing dose-  
intense therapy in cancer patients by protecting normal cells and  
preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
shown in the specification but was derived from the TS wild-type  
sequence, also not given in the specification  
XX Sequence 313 AA;  
SQ Score 56; DB 2; Length 313;  
Query Match 100.0%; Score 56; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LMALPPCHAL 10  
Db 189 LMALPPCHAL 198



RESULT 15 AAW75768 standard; protein; 313 AA.

ID AAW75768;  
XX  
AC AAW75768;  
XX DT 19-NOV-1998 (first entry)  
XX DB Mutated thymidylate synthase.  
XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Fdurd;  
KW tomudex; gene therapy; cancer; myelotoxicity.  
XX OS Homo sapiens.  
OS Synthetic.  
XX Key FH Misc-difference 225  
FT Location/Qualifiers /note= "Wild-type Phe substituted by Tyr"  
XX PN WO9833518-A1.  
XX PD 06-AUG-1998.  
XX PF 03-FEB-1998; 98WO-US002145.  
XX PR 04-FEB-1997; 97US-0037163P.  
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
XX DR WPI; 1998-437173/37.  
XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
PT for use in gene therapy and for treating cancers.  
XX PS Claim 6; Page: 78pp; English.  
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
CC most of which were generated by using site directed mutagenesis. This was  
CC performed by creating a TS expression vector pcDNA3hts which contained  
CC the human TS gene coding sequence, and using this to produce ssDNA for  
CC site-directed mutagenesis and sequence analysis. Mutants which were not  
CC created this way were produced by random mutagenesis, by exposing human  
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
CC selection. From these mutagenesis experiments, 17 different mutants were  
CC obtained, each of which were mutated at one of five different amino acid  
CC positions causing an amino acid change and thus causing the TS enzyme to  
CC have different properties. It was found that mutations at positions 49  
CC and 52 caused the enzyme to form resistance to AG337 and Fdurd, whereas  
CC mutations at 108 were found to confer tomudex and AG337 resistance. In  
CC general mutated TS cDNAs have been found to be resistant to TS specific  
CC inhibitors, and to have a high catalytic efficiency and good stability.  
CC The mutant TS cDNA can be used in gene therapy to transfer drug  
CC resistance to human haematopoietic progenitors, thus allowing dose-  
CC intense therapy in cancer patients by protecting normal cells and  
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
CC shown in the specification but was derived from the TS wild-type  
CC sequence, also not given in the specification  
XX Sequence 313 AA;

RESULT 16 AAW75762 standard; protein; 313 AA.

ID AAW75762;  
XX AC AAW75762;  
XX DT 19-NOV-1998 (first entry)  
XX DB Mutated thymidylate synthase.  
XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Fdurd;  
KW tomudex; gene therapy; cancer; myelotoxicity.  
XX OS Homo sapiens.  
OS Synthetic.  
XX Key FH Misc-difference 221  
FT Location/Qualifiers /note= "Wild-type Leu substituted by Ala"  
XX PN WO9833518-A1.  
XX PD 06-AUG-1998.  
XX PF 03-FEB-1998; 98WO-US002145.  
XX PR 04-FEB-1997; 97US-0037163P.  
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
XX DR WPI; 1998-437173/37.  
XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
PT for use in gene therapy and for treating cancers.  
XX PS Claim 5; Page: 78pp; English.  
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
CC most of which were generated by using site directed mutagenesis. This was  
CC performed by creating a TS expression vector pcDNA3hts which contained  
CC the human TS gene coding sequence, and using this to produce ssDNA for  
CC site-directed mutagenesis and sequence analysis. Mutants which were not  
CC created this way were produced by random mutagenesis, by exposing human  
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
CC selection. From these mutagenesis experiments, 17 different mutants were  
CC obtained, each of which were mutated at one of five different amino acid  
CC positions causing an amino acid change and thus causing the TS enzyme to  
CC have different properties. It was found that mutations at positions 49  
CC and 52 caused the enzyme to form resistance to AG337 and Fdurd, whereas  
CC mutations at 108 were found to confer tomudex and AG337 resistance. In  
CC general mutated TS cDNAs have been found to be resistant to TS specific  
CC inhibitors, and to have a high catalytic efficiency and good stability.  
CC The mutant TS cDNA can be used in gene therapy to transfer drug  
CC resistance to human haematopoietic progenitors, thus allowing dose-  
CC intense therapy in cancer patients by protecting normal cells and  
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
CC shown in the specification but was derived from the TS wild-type  
CC sequence, also not given in the specification  
XX Sequence 313 AA;

Query Match	Score 56;	DB 2;	Length 313;
Best Local Similarity	100.0%;	Pred. No. 0.55;	Matches 10;
Matches	10;	Mismatches 0;	Indels 0;
Conservative	0;	Gaps 0;	Gaps 0;
Qy	1 LMALPPCHAL 10		
Db	189 LMALPPCHAL 198		

RESULT 17	AAW75756	AAW75756 standard; protein; 313 AA.	RESULT 18	AAW75759	AAW75759 standard; protein; 313 AA.
ID	AAW75756		ID	AAW75759	
XX			XX		
AC	AAW75756;		AC	AAW75759;	
XX	DT 19-NOV-1998 (first entry)		XX	DT 19-NOV-1998 (first entry)	
DB	Mutated thymidylate synthase.		DB	Mutated thymidylate synthase.	
XX	KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts; random mutagenesis; sarcoma HT1080 cell; alkylating agent ; AG337; Ptdrd; tomudex; gene therapy; cancer; myelotoxicity.		XX	KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts; random mutagenesis; sarcoma HT1080 cell; alkylating agent ; AG337; Ptdrd; tomudex; gene therapy; cancer; myelotoxicity.	
KW			KW		
XX	Homo sapiens.		XX	Homo sapiens.	
OS	Synthetic.		OS	Synthetic.	
XX			XX		
Key	Location/Qualifiers		Key	Location/Qualifiers	
PH			PH		
FT	Misc-difference 108 /note= "Wild-type Ile substituted by Phe"		FT	Misc-difference 108 /note= "Wild-type Ile substituted by Asn."	
XX	PN WO9833518-A1.		XX	PN WO9833518-A1.	
XX	PD 06-AUG-1998.		XX	PD 06-AUG-1998.	
XX	PF 03-FEB-1998; 98WO-US002145.		XX	PF 03-FEB-1998; 98WO-US002145.	
XX	PR 04-FEB-1997; 97US-0037163P.		XX	PR 04-FEB-1997; 97US-0037163P.	
XX	PA (SLOK ) SLOAN KETTERING INST CANCER RES.		XX	PA (SLOK ) SLOAN KETTERING INST CANCER RES.	
XX	PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;		XX	PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;	
XX	DR 1998-437173/37.		XX	DR 1998-437173/37.	
XX	New mutant human thymidylate synthases - used to, e.g. develop products for use in gene therapy and for treating cancers.		XX	New mutant human thymidylate synthases - used to, e.g. develop products for use in gene therapy and for treating cancers.	
PT			PT		
XX	PS Claim 4; Page: 78pp; English.		XX	PS Claim 4; Page: 78pp; English.	
XX	Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants most of which were generated by using site directed mutagenesis. This was performed by creating a TS expression vector pcDNA3hts which contained the human TS gene coding sequence, and using this to produce sDNA for site-directed mutagenesis and sequence analysis. Mutants which were not created this way were produced by random mutagenesis, by exposing human sarcoma HT1080 cells to an alkylating agent and then using AG337 for selection. From these mutagenesis experiments, 17 different mutants were obtained, each of which were mutated at one of five different amino acid positions causing an amino acid change and thus causing the TS enzyme to have different properties. It was found that mutations at positions 49 and 52 caused the enzyme to form resistance to AG337 and Ptdrd, whereas mutations at 108 were found to confer tomudex and AG337 resistance. In general mutated TS cDNAs have been found to be resistant to TS specific inhibitors, and to have a high catalytic efficiency and good stability. The mutant TS cDNA can be used in gene therapy to transfer drug resistance to human haemopoietic progenitors, thus allowing dose-intense therapy in cancer patients by protecting normal cells and preventing dose-limiting myelotoxicity. N.B. The present sequence is not shown in the specification but was derived from the TS wild-type sequence, also not given in the specification		XX	Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants most of which were generated by using site directed mutagenesis. This was performed by creating a TS expression vector pcDNA3hts which contained the human TS gene coding sequence, and using this to produce sDNA for site-directed mutagenesis and sequence analysis. Mutants which were not created this way were produced by random mutagenesis, by exposing human sarcoma HT1080 cells to an alkylating agent and then using AG337 for selection. From these mutagenesis experiments, 17 different mutants were obtained, each of which were mutated at one of five different amino acid positions causing an amino acid change and thus causing the TS enzyme to have different properties. It was found that mutations at positions 49 and 52 caused the enzyme to form resistance to AG337 and Ptdrd, whereas mutations at 108 were found to confer tomudex and AG337 resistance. In general mutated TS cDNAs have been found to be resistant to TS specific inhibitors, and to have a high catalytic efficiency and good stability. The mutant TS cDNA can be used in gene therapy to transfer drug resistance to human haemopoietic progenitors, thus allowing dose-intense therapy in cancer patients by protecting normal cells and preventing dose-limiting myelotoxicity. N.B. The present sequence is not shown in the specification but was derived from the TS wild-type sequence, also not given in the specification	
CC	Sequence 313 AA;		CC	Sequence 313 AA;	
PS			PS		
XX	Query Match 100.0%; Score 56; DB 2; Length 313;		XX	Query Match 100.0%; Score 56; DB 2; Length 313;	
CC	Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;		CC	Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;	
CC	Matches 10; Conservative 0; MisMatches 0; Gaps 0;		CC	Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;	
Qy	1 LMALPPCHAL 10		Qy	1 LMALPPCHAL 10	
Db	189 LMALPPCHAL 198		Db	189 LMALPPCHAL 198	

**RESULT 19**  
 AAW75767 standard; protein; 313 AA.  
 ID AAW75767;  
 XX  
 AC AAW75767;  
 XX  
 DT 19-NOV-1998 (first entry)  
 XX  
 DE Mutated thymidylate synthase.  
 XX  
 Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 tomudex; gene therapy; cancer; myelotoxicity.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FH Misc-difference 225  
 FT /note= "Wild-type Phe substituted by Leu"  
 XX  
 PN WO9833518-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PP 03-FEB-1998; 98WO-US002145.  
 XX  
 PR 04-FEB-1997; 97US-0037163P.  
 XX  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX  
 PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 XX  
 DR WPI; 1998-437173/37.  
 XX  
 PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 XX  
 PS Claim 6 ; Page; 78pp; English.  
 XX  
 Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 CC most of which were generated by using site directed mutagenesis. This was  
 CC performed by creating a TS expression vector pcDNA3hts which contained  
 CC the human TS gene coding sequence, and using this to produce ssDNA for  
 CC site-directed mutagenesis and sequence analysis. Mutants which were not  
 CC created this way were produced by random mutagenesis, by exposing human  
 CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
 CC selection. From these mutagenesis experiments, 17 different mutants were  
 CC obtained, each of which were mutated at one of five different amino acid  
 CC positions causing an amino acid change and thus causing the TS enzyme to  
 CC have different properties. It was found that mutations at positions 49  
 CC and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 CC mutations at 108 were found to confer tomude and AG337 resistance. In  
 CC general mutated TS cDNAs have been found to be resistant to TS specific  
 CC inhibitors, and to have a high catalytic efficiency and good stability.  
 CC The mutant TS cDNA can be used in gene therapy to transfer drug  
 CC resistance to human haematopoietic progenitors, thus allowing dose-  
 CC intensive therapy in cancer patients by protecting normal cells and  
 CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 CC shown in the specification but was derived from the TS wild-type  
 CC sequence, also not given in the specification  
 XX  
 Sequence 313 AA;

**RESULT 20**  
 AAW75760  
 ID AAW75760 Standard; protein; 313 AA.  
 XX  
 AC AAW75760;  
 XX  
 DT 19-NOV-1998 (first entry)  
 XX  
 DE Mutated thymidylate synthase.  
 XX  
 Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 KW tomudex; gene therapy; cancer; myelotoxicity.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FH Misc-difference 221  
 FT /note= "Wild-type Leu substituted by Phe"  
 XX  
 PN WO9833518-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PP 03-FEB-1998; 98WO-US002145.  
 XX  
 PR 04-FEB-1997; 97US-0037163P.  
 XX  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX  
 PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 XX  
 DR WPI; 1998-437173/37.  
 XX  
 PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 XX  
 PS Claim 5 ; Page; 78pp; English.  
 XX  
 Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 CC most of which were generated by using site directed mutagenesis. This was  
 CC performed by creating a TS expression vector pcDNA3hts which contained  
 CC the human TS gene coding sequence, and using this to produce ssDNA for  
 CC site-directed mutagenesis and sequence analysis. Mutants which were not  
 CC created this way were produced by random mutagenesis, by exposing human  
 CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
 CC selection. From these mutagenesis experiments, 17 different mutants were  
 CC obtained, each of which were mutated at one of five different amino acid  
 CC positions causing an amino acid change and thus causing the TS enzyme to  
 CC have different properties. It was found that mutations at positions 49  
 CC and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 CC mutations at 108 were found to confer tomude and AG337 resistance. In  
 CC general mutated TS cDNAs have been found to be resistant to TS specific  
 CC inhibitors, and to have a high catalytic efficiency and good stability.  
 CC The mutant TS cDNA can be used in gene therapy to transfer drug  
 CC resistance to human haematopoietic progenitors, thus allowing dose-  
 CC intensive therapy in cancer patients by protecting normal cells and  
 CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 CC shown in the specification but was derived from the TS wild-type  
 CC sequence, also not given in the specification  
 XX  
 Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 21  
 AAW75761  
 ID AAW75761 standard; protein; 313 AA.  
 XX  
 AC AAW75761;  
 XX DT 19-NOV-1998 (first entry)  
 DE Mutated thymidylate synthase.  
 XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 tomudex; gene therapy; cancer; myelotoxicity.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX Key  
 PH Location/Qualifiers  
 FT Misc-difference 221 /note= "Wild-type Leu substituted by Arg"  
 XX WO9833518-A1.  
 PN XX  
 PD 06-AUG-1998.  
 PP XX  
 PR 03-FEB-1998; 98WO-US002145.  
 PR XX  
 PR 04-FEB-1997; 97US-0037163P.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 PA DR  
 PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 XX DR WPI: 1998-437173/37.  
 XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 PT XX  
 PS Claim 5; Page: 78pp; English.  
 XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 CC most of which were generated by using site directed mutagenesis. This was  
 CC performed by creating a TS expression vector pcDNA3hts which contained  
 CC the human TS gene coding sequence, and using this to produce sDNA for  
 CC site-directed mutagenesis and sequence analysis. Mutants which were not  
 CC created this way were produced by random mutagenesis, by exposing human  
 CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
 CC selection. From these mutagenesis experiments, 17 different mutants were  
 CC obtained, each of which were mutated at one of five different amino acid  
 CC positions causing an amino acid change and thus causing the TS enzyme to  
 CC have different properties. It was found that mutations at positions 49  
 CC and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 CC mutations at 108 were found to confer tomude and AG337 resistance. In  
 CC general mutated TS cDNAs have been found to be resistant to TS specific  
 CC inhibitors, and to have a high catalytic efficiency and good stability.  
 CC The mutant TS cDNA can be used in gene therapy to transfer drug  
 CC resistance to human haematopoietic progenitors, thus allowing dose-  
 CC intensive therapy in cancer patients by protecting normal cells and  
 CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 CC shown in the specification but was derived from the TS wild-type  
 CC sequence, also not given in the specification  
 XX SQ Sequence 313 AA;

RESULT 22  
 AAW75753  
 ID AAW75753 standard; protein; 313 AA.  
 XX  
 AC AAW75753;  
 XX DT 19-NOV-1998 (first entry)  
 DE Mutated thymidylate synthase.  
 XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hts;  
 random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; Edurd;  
 KW tomudex; gene therapy; cancer; myelotoxicity.  
 XX OS Homo sapiens.  
 XX FH Key  
 FT Misc-difference 49 /note= "Wild-type Asp substituted by Gly"  
 XX WO9833518-A1.  
 PN XX  
 PD 06-AUG-1998.  
 PP XX  
 PR 03-FEB-1998; 98WO-US002145.  
 PR XX  
 PR 04-FEB-1997; 97US-0037163P.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 PA DR  
 PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;  
 XX DR WPI: 1998-437173/37.  
 XX PT New mutant human thymidylate synthases - used to, e.g. develop products  
 PT for use in gene therapy and for treating cancers.  
 PT XX  
 PS Claim 2; Page: 78pp; English.  
 XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants  
 CC most of which were generated by using site directed mutagenesis. This was  
 CC performed by creating a TS expression vector pcDNA3hts which contained  
 CC the human TS gene coding sequence, and using this to produce sDNA for  
 CC site-directed mutagenesis and sequence analysis. Mutants which were not  
 CC created this way were produced by random mutagenesis, by exposing human  
 CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for  
 CC selection. From these mutagenesis experiments, 17 different mutants were  
 CC obtained, each of which were mutated at one of five different amino acid  
 CC positions causing an amino acid change and thus causing the TS enzyme to  
 CC have different properties. It was found that mutations at positions 49  
 CC and 52 caused the enzyme to form resistance to AG337 and Edurd, whereas  
 CC mutations at 108 were found to confer tomude and AG337 resistance. In  
 CC general mutated TS cDNAs have been found to be resistant to TS specific  
 CC inhibitors, and to have a high catalytic efficiency and good stability.  
 CC The mutant TS cDNA can be used in gene therapy to transfer drug  
 CC resistance to human haematopoietic progenitors, thus allowing dose-  
 CC intensive therapy in cancer patients by protecting normal cells and  
 CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not  
 CC shown in the specification but was derived from the TS wild-type  
 CC sequence, also not given in the specification  
 XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; SQ 1 LMALPPCHAL 10  
 Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 23  
 ABP53744 standard; protein: 313 AA.  
 ID ABP53744;  
 AC ABP53744;  
 XX 02-JAN-2003 (first entry)  
 DE Human thymidylate synthase SEQ ID NO:14.  
 KW Thymidylate synthase; enzyme; binding; neoplastic disorder;  
 KW chemotherapeutic; cytostatic; thymidylate synthase inhibitor; cancer.  
 OS Homo sapiens.  
 XX WO200210366-A2.  
 PN 07-FEB-2002.  
 XX 02-AUG-2001; 2001WO-US024417.  
 PP 02-AUG-2000; 2000US-00631275.  
 PR 28-NOV-2000; 2000US-00722544.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA (RGPC ) UNTV CALIFORNIA.  
 XX PI Chen H, Freimer NB, Novak T;  
 DR WPI; 2002-195962/25.  
 DR N-PSDB; ABK43335.  
 XX PT New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for screening for molecules which modulate HKNG1 expression for the treatment of bipolar disorder and schizophrenia.  
 XX Disclosure; Fig 45; 367pp; English.  
 XX The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene product. The human gene for HKNG1 is located on chromosome 18p in an area associated with bipolar affective disorder. BAD. Also included are an expression vector comprising the nucleic acid, a host cell expressing the nucleic acid, an anti-HKNG1 antibody, a method of identifying modulators of HKNG1, and identifying an individual, (at risk of) having HKNG1-mediated disorder comprising detecting the presence or absence of a polymorphism that correlates with an HKNG1 allele associated with the disorder, where the presence of the polymorphism indicates that the individual (is at risk of) having HKNG1-mediated disorder. A (small molecule) compound which modulates (inhibits or potentiates) expression of a HKNG1 gene or gene product in a human individual is useful for the treatment of a HKNG1-mediated disorder such as bipolar affective disorder (BAD), severe bipolar affective (mood) disorder (BP-I) and schizophrenia. The present sequence is the thymidylate synthase, TS, protein. The gene for TS overlaps that of HKNG1 and therefore TS may also be involved in the diseases listed above  
 XX Sequence 313 AA;  
 SQ Query Match 100.0%; Score 56; DB 5; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Gaps 0;  
 Db 189 LMALPPCHAL 198  
 RESULT 24  
 ADC56778 standard; protein: 313 AA.  
 ID ADC56778;  
 AC ADC56778;  
 XX  
 RESULT 25  
 ADC56778  
 ID ADC56778 standard; protein: 313 AA.  
 AC ADC56778;

DT	18-DEC-2003	(first entry)	XX	24-JUN-2002;	2002JP-00183603.
DB	Human thymidylic acid synthetase protein.	XX	XX	PR	25-JUN-2001;
KW	human; thymidylic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.	XX	XX	PR	001JP-001974.
XX		XX	XX	PA	(ITOY/) ITO Y.
OS	Homo sapiens.	XX	XX	PA	
XX	WPI;	2003-611129/58.	DR		
PN	JP2003102480-A.	XX	XX		
XX	Novel tumor antigenic peptide or polypeptide useful for inducing	XX	XX		
PD	cytotoxic T cells or for treating cancer such as colon, mouth, lung,	XX	XX		
XX	prostatic or gynecological cancer.	XX	XX		
PF	28-SEP-2001;	2001JP-00300086.	PS	Claim 2;	SEQ ID NO 74; 98pp; Japanese.
XX	PR	28-SEP-2001;	2001JP-00300086.	XX	The invention relates to a novel tumour antigenic peptide or polypeptide comprising a sequence selected from 99 sequences fully defined in the specification. The tumour antigenic peptide or polypeptide comprises a sequence selected from 99 sequences fully defined in the specification, where the tumour antigenic peptide preferably has a sequence of Glu-Pro-Glu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a sequence comprising 393 amino acids fully defined in the specification. The invention further provides a cancer vaccine comprising a tumour antigenic peptide or polypeptide, which has cytotoxic activity. A tumour antigenic peptide, polypeptide, its encoding polynucleotide, a hybridising polynucleotide, a recombinant vector containing the polynucleotide, a host transformed with the vector or an antibody are useful for screening for compounds that interact with the tumour antigenic peptide, the polypeptide or its encoding polynucleotide and increases the expression of the tumour antigenic peptide or the polypeptide is useful for inducing cytotoxic T cells. The tumour antigenic peptide vaccine is useful for treating cancer such as colon, mouth, lung, prostatic or gynecological cancer. The invention also provides a pharmaceutical composition useful for treating cancer. The tumour antigenic peptide or the polypeptide is useful as an antigen to create antibodies. This sequence represents one of the tumour antigenic peptides of the invention.
PA	(SRLS-) SRL KK.	XX	XX	CC	
XX	Measuring human thymidylic-acid synthetase mRNA, by using primers that hybridize to full length cDNA of thymidylic-acid synthetase gene but does not hybridize to variant cDNA in which specific exons of gene are deleted.	XX	XX	CC	
PS	Disclosure; Page 17-18; 28pp; Japanese.	XX	XX	CC	
XX	This invention relates to a novel method for measuring human thymidylic acid synthetase (hts) mRNA (EC 2.1.1.45). Specifically, it comprises amplifying cDNA or mRNA of the hts gene using forward and reverse primers, where the forward primer does not hybridize to the variant cDNA in which exon 2 and exon 3 of the gene are deleted. Likewise the reverse primer does not hybridize to the variant cDNA in which exon 4 of the hts gene has been deleted. Accordingly, by measuring the amplified product of human thymidylic acid synthetase it is possible to exactly measure only the active hts enzyme product, which is useful in the prognosis or treatment of cancer. Furthermore, the throughput of hts in a cancer cell can estimate the therapeutic effect of an anticancer agent. This polypeptide sequence is the human thymidylic acid synthetase protein of the invention. NOTE: This protein is not further described in the specification but is given as an embedded protein in the sequence listing.	XX	XX	CC	
XX	XX	XX	XX	CC	
SQ	Sequence 313 AA;	XX	XX	CC	
Query Match	100.0%	Score 56;	DB 7;	Length 313;	
Best Local Similarity	100.0%	Pred. No. 0.55;	Pred. No. 0.55;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	189 LMALPPCHAL 198	XX	XX	XX	
Qy	1 LMALPPCHAL 10	XX	XX	XX	
Db	189 LMALPPCHAL 198	XX	XX	XX	
RESULT 27		DT	29-JAN-2004	(first entry)	
ID	ADD2244 standard; protein; 313 AA.	XX	XX	XX	
XX	Human thymidylate synthase mutant enzyme 24.	XX	XX	XX	
AC	ADD2244;	XX	XX	XX	
XX	thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; chemotherapy; thymidylate synthase inhibitor; early progenitor cell; cytotoxic; human mucosa ulceration; gene therapy; human; enzyme; mutant; mutagen; 5-fluorouridine; 5-FdUUR.	XX	XX	XX	
DT	15-JAN-2004 (first entry)	XX	XX	XX	
DB	HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ NO 74.	XX	XX	XX	
XX	tumour antigenic peptide; cancer; vaccine; cytotoxic; cytotoxic T cell; colon; mouth; lung; prostatic; gynecological; human.	XX	XX	XX	
KW	Homo sapiens.	XX	XX	XX	
XX	JP2003111595-A.	XX	XX	XX	
PN		FT		Misc-difference 103 /note= "Wild-type Ser replaced by Thr"	
XX		FT		Misc-difference 204 /note= "Wild-type Val replaced by Ala"	
PD	15-APR-2003.	FT			



KW mutein; 5-fluorouridine; 5-FdUR.  
 XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 OS KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 Synthetic. KW cytotoxic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 OS Homo sapiens. KW mutein; 5-fluorouridine; 5-FdUR.

XX  
 FH Synthetic.  
 Key  
 FT Homo sapiens.  
 Location/Qualifiers  
 FT  
 Misc-difference 84  
 /note= "Wild-type Val replaced by Ala"  
 XX  
 PN EP1316604-A1.  
 XX  
 PD 04-JUN-2003.  
 XX  
 PP 29-JUN-2002; 2002EP-00014489.  
 XX  
 PR 03-DEC-2001; 2001US-0334557P.  
 XX  
 PA (GEURTSEN W.)  
 XX  
 PI Loeb L, Geurtzen W;  
 XX  
 DR WPI; 2003-495241/47.  
 XX  
 PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 XX  
 PS Claim 2; Page: 36pp; English.  
 XX  
 CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa against the toxic effects of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displays resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX  
 SQ Sequence 313 AA;

Query Match	100.0%	Score 56;	DB 7;	Length 313;
Best Local Similarity	100.0%	Pred. No. 0.55;	Indels	0;
Matches	10;	Conservative	0;	Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 30  
 ADE76336  
 ID ADE76636 Standard; protein; 313 AA.  
 XX  
 AC ADE76636;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human thymidylate synthase mutant enzyme 11.  
 XX

XX  
 FH  
 Key  
 FT  
 Misc-difference 250  
 /note= "Wild-type His replaced by Leu"  
 XX  
 PN EP1316604-A1.  
 XX  
 PD 04-JUN-2003.  
 XX  
 PP 29-JUN-2002; 2002EP-00014489.  
 XX  
 PR 03-DEC-2001; 2001US-0334557P.  
 XX  
 PA (GEURTSEN W.)  
 XX  
 PI Loeb L, Geurtzen W;  
 XX  
 DR WPI; 2003-495241/47.  
 XX  
 PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 XX  
 PS Claim 2; Page: 36pp; English.  
 XX  
 CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa against the toxic effects of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displays resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX  
 SQ Sequence 313 AA;

Query Match	100.0%	Score 56;	DB 7;	Length 313;
Best Local Similarity	100.0%	Pred. No. 0.55;	Indels	0;
Matches	10;	Conservative	0;	Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 31  
 ADE7643  
 ID ADE76643 Standard; protein; 313 AA.  
 XX  
 AC ADE76643;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human thymidylate synthase mutant enzyme 11.  
 XX

RESULT 32  
 ADB76626 standard; protein: 313 AA.  
 ID ADB76626;  
 XX AC ADB76626;  
 XX DR 29-JAN-2004 (first entry)  
 XX DB Human thymidylate synthase mutant enzyme 1.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 55 /note= "Wild-type Thr replaced by Ile"  
 FT Misc-difference 106 /note= "Wild-type Val replaced by Ala"  
 FT Misc-difference 284 /note= "Wild-type Lys replaced by Ile"  
 XX EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PP 29-JUN-2002; 2002EP-00014499.  
 XX PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSEN W.  
 XX PI Loeb L, Geurtzen W;  
 XX DR WPI; 2003-495241/47.  
 PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wild-type thymidylate synthase in single, double or multiple mutations.  
 XX PS Claim 4: Page: 36pp; English.  
 CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 Sequence 313 AA;  
 Query Match 100.0%; Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Sq 1 LMALPPCHAL 10  
 Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198  
 XX Sequence 313 AA;  
 XX Query Match 100.0%; Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LMALPPCHAL 10  
 Db |||||

Db 189 LMALPPCHAL 198 Query Match 100.0%; Score 56; DB 7; Length 313;  
 RESULT 33 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 ADE7647 ID 1 LMALPPCHAL 10  
 XX ADE7647 standard; protein; 313 AA.  
 AC ADE7647; Qy 1 LMALPPCHAL 10  
 XX ADE7647; Db 189 LMALPPCHAL 198

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DT 29-JAN-2004 (first entry) RESULT 34  
 XX Human thymidylate synthase mutant enzyme 22.  
 DB Human thymidylate synthase mutant enzyme 22. ADE76654 standard; protein; 313 AA.  
 XX ADE76654; ID ADE76654; Location/Qualifiers  
 KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 KW mutant; 5-Fluorouridine; 5-FdUR.  
 XX OS Human thymidylate synthase mutant enzyme 29.  
 OS Synthetic. KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 OS Homo sapiens. KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 KW mutant; 5-Fluorouridine; 5-FdUR.

---

XX Key-Difference 6 /note= "Wild-type Ser replaced by Asn"  
 FT Misc-difference 69 /note= "Wild-type Asp replaced by Gln"  
 FT Misc-difference 211 /note= "Wild-type Gln replaced by Leu"  
 PN EP13116604-A1. XX Key-Difference 38 /note= "Wild-type Gln replaced by His"  
 PD 04-JUN-2003. FT Misc-difference 104 /note= "Wild-type Lys replaced by Asp"  
 XX FF EP13116604-A1. XX Key-Difference 38 /note= "Wild-type Gln replaced by His"  
 XX PR 03-DEC-2001; 2001US-0334557P. XX FF EP13116604-A1.  
 XX DR WPI: 2003-495241/47. XX PD 04-JUN-2003.  
 XX PI Loeb L; Geurtzen W. XX PR 03-DEC-2001; 2001US-0334557P.  
 XX DR WPI: 2003-495241/47. XX PA (GEUR/) GEURTSEN W.  
 XX PT New thymidylate synthase mutant, useful for protecting normal cell XX PA (GEUR/) GEURTSEN W.  
 PT populations against toxicity from thymidylate synthase inhibitors, or XX PI Loeb L; Geurtzen W;  
 PT differs from human wildtype thymidylate synthase in single, double or XX DR WPI: 2003-495241/47.  
 PT multiple mutations. XX PA (GEUR/) GEURTSEN W.  
 XX PS Claim 4; Page: 36pp; English. XX New thymidylate synthase mutant, useful for protecting normal cell  
 XX This invention relates to a novel thymidylate synthase mutant that XX populations against toxicity from thymidylate synthase in single, double or  
 CC differs from human wild-type thymidylate synthase by one, two or more XX multiple mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a  
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a XX result interfere with the DNA-metabolism of tumour cells. The protein  
 CC mutant is useful for the transfection of human cells which may be XX affected by side effects due to chemotherapy with thymidylate synthase  
 CC inhibitors, for the ex-vivo or in vivo transfection of early progenitor cells separated or grown from XX bone marrow cells. The protein mutant is also used for identifying new  
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for XX protecting human cell populations, preferably mucosa, against the toxic  
 CC manifestations of analogues that inhibit thymidylate synthase, or for XX manufacturing cytostatic pharmaceutical and gene therapeutic compositions  
 CC for the protection of human mucosa against ulceration under chemotherapy  
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the  
 CC mutant protein of the invention can also be used in gene therapy. The  
 CC present sequence is that of a mutant human thymidylate synthase (TS)  
 CC enzyme of the invention which displays resistance to the TS-inhibitor  
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in  
 CC the specification but was created by the indexer from information given in  
 CC the claims and the wild-type human TS sequence.  
 XX Sequence 313 AA;

CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the  
 CC specification but was created by the indexer from information given in the  
 CC claims and the wild-type human TS sequence.

XX Sequence 313 AA;  
 SQ      Query Match      Score 56; DB 7; Length 313;  
 XX      Best Local Similarity 100.0%; Pred. No. 0.55;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy      1 LMALPPCHAL 10  
 Db      189 LMALPPCHAL 198

RESULT 35  
 ADB7655      Query Match      Score 56; DB 7; Length 313;  
 ID ADB7655 standard; protein; 313 AA.  
 XX  
 AC ADE76655;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX Human thymidylate synthase mutant enzyme 30.  
 DB thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 KW cytosstatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 KW mutagen; 5-Fluorouridine; 5-FdUR.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/qualifiers  
 FT Misc-difference 8 /note= "Wild-type Leu replaced by Gln"  
 FT Misc-difference 81 /note= "Wild-type Trp replaced by Gly"  
 FT Misc-difference 131 /note= "Wild-type Leu replaced by Val"  
 FT Misc-difference 230 /note= "Wild-type Tyr replaced by Phe"  
 PT EP1316604-A1.  
 PN  
 XX  
 PD 04-JUN-2003.  
 XX  
 PP 29-JUN-2002; 2002EP-00014489.  
 XX  
 PR 03-DEC-2001; 2001US-0334557P.  
 XX  
 PA (GEUR/)  
 XX  
 PI Loeb L, Geurtzen W.  
 XX  
 DR WPI; 2003-495241/47.

New thymidylate synthase mutant, useful for protecting normal cell  
 PT populations against toxicity from thymidylate synthase inhibitors,  
 PT differs from human wildtype thymidylate synthase in single, double or  
 PT multiple mutations.  
 XX  
 PS Claim 4; Page: 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that  
 CC differs from human wild-type thymidylate synthase by one, two or more  
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a  
 CC result interfere with the DNA-metabolism of tumour cells. The protein  
 CC mutant is useful for the transfection of human cells which may be  
 CC affected by side effects due to chemotherapy with thymidylate synthase  
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,  
 CC or for transfection of early progenitor cells separated or grown from  
 CC bone marrow cells. The protein mutant is also used for identifying new

CC nucleotide analogues that inhibit normal human thymidylate synthase, for  
 CC protecting human cell populations, preferably mucosa, against the toxic  
 CC manifestation of analogues that inhibit thymidylate synthase, or for  
 CC manufacturing cytostatic pharmaceutical compositions  
 CC for the protection of human mucosa against ulceration under chemotherapy  
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the  
 CC mutant protein of the invention can also be used in gene therapy. The  
 CC present sequence is that of a mutant human thymidylate synthase (TS)  
 CC enzyme of the invention which displayed resistance to the TS-inhibitor  
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the  
 CC specification but was created by the indexer from information given in the  
 CC claims and the wild-type human TS sequence.  
 XX  
 SQ Sequence 313 AA;

RESULT 36  
 ADB76648      Query Match      100.0%; Score 56; DB 7; Length 313;  
 ID ADB76648 standard; protein; 313 AA.  
 XX  
 AC ADE76648;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX Human thymidylate synthase mutant enzyme 23.  
 DE Human thymidylate synthase mutant enzyme 23.  
 XX  
 FH Key Location/qualifiers  
 FT Misc-difference 5 /note= "Wild-type Gly replaced by Asp"  
 FT Misc-difference 13 /note= "Wild-type Leu replaced by Arg"  
 FT Misc-difference 231 /note= "Wild-type Ala replaced by Thr"  
 XX  
 PN EP1316604-A1.  
 XX  
 PD 04-JUN-2003.  
 XX  
 PP 29-JUN-2002; 2002EP-00014489.  
 XX  
 PR 03-DEC-2001; 2001US-0334557P.

XX  
 PA (GEUR/)  
 XX  
 PI Loeb L, Geurtzen W.  
 XX  
 DR WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell  
 PT populations against toxicity from thymidylate synthase inhibitors,  
 PT differs from human wildtype thymidylate synthase in single, double or  
 PT multiple mutations.  
 XX  
 PS Claim 4; Page: 36pp; English.

XX New thymidylate synthase mutant, useful for protecting normal cell  
 PT populations against toxicity from thymidylate synthase inhibitors,  
 PT differs from human wildtype thymidylate synthase in single, double or  
 PT multiple mutations.  
 XX  
 PS Claim 4; Page: 36pp; English.  
 XX  
 CC This invention relates to a novel thymidylate synthase mutant that  
 CC differs from human wild-type thymidylate synthase by one, two or more  
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a  
 CC result interfere with the DNA-metabolism of tumour cells. The protein  
 CC mutant is useful for the transfection of human cells which may be  
 CC affected by side effects due to chemotherapy with thymidylate synthase  
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,  
 CC or for transfection of early progenitor cells separated or grown from  
 CC bone marrow cells. The protein mutant is also used for identifying new

CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a CC result interfere with the DNA-metabolism of tumour cells. The protein CC mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, CC or for transfection of early progenitor cells separated or grown from CC bone marrow cells. The protein mutant is also used for identifying new CC nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic CC manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions CC for the protection of human mucosa against ulceration under chemotherapy CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the CC mutant protein of the invention can also be used in gene therapy. The CC present sequence is that of a mutant human thymidylate synthase (TS) CC enzyme of the invention which displayed resistance to the TS-inhibitor CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the CC specification but was created by the indexer from information given in the CC claims and the wild-type human TS sequence.

XX Sequence 313 AA;

Query Match Score 56; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55%;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
Db 189 LMALPPCHAL 198

RESULT 37  
ADE76651 ID ADE76651 standard; protein; 313 AA.  
XX AC ADE76651;  
XX DT 29-JAN-2004 (first entry)

XX Human thymidylate synthase mutant enzyme 26.  
XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; KW

KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell; KW cytosstatic; human mucosa ulceration; gene therapy; human; enzyme; mutant; KW mutant; 5-Fluorouridine; 5-FdUR.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 17  
FT /note= "Wild-type Ala replaced by Thr"

FT Misc-difference 116  
FT /note= "Wild-type Asp replaced by Ala"

FT Misc-difference 254  
FT /note= "Wild-type Asp replaced by Glu"

XX PN EP1316604-A1.  
XX PD 04-JUN-2003.  
XX PR 29-JUN-2002; 2002EP-00014489.  
XX PA (GEUR/) GEURTSEN W.  
XX PI Loeb L, Geurtzen W;  
XX DR WPI; 2003-495241/47.  
XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors.

differs from human wildtype thymidylate synthase in single, double or multiple mutations.

PT XX  
PT PS  
Claim 4: Page: 36pp; English.

This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match Score 56; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55%;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
Db 189 LMALPPCHAL 198

RESULT 38

ADE76651 ID ADE76651 standard; protein; 313 AA.  
XX AC ADE76651;  
XX DT 29-JAN-2004 (first entry)

XX Human thymidylate synthase mutant enzyme 12.  
XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell; KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant; KW mutant; 5-Fluorouridine; 5-FdUR.

XX OS Synthetic.  
OS Homo Sapiens.

XX Key Location/Qualifiers  
FT Misc-difference 254  
FT /note= "Wild-type Asp replaced by Glu"  
XX PN EP1316604-A1.  
XX PD 04-JUN-2003.  
XX PR 29-JUN-2002; 2002EP-00014489.  
XX PA (GEUR/) GEURTSEN W.  
XX PI Loeb L, Geurtzen W;  
XX DR WPI; 2003-495241/47.  
XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors.

PT XX  
PT PS  
Claim 4: Page: 36pp; English.

XX SQ Sequence 313 AA;

Query Match Score 56; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55%;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
Db 189 LMALPPCHAL 198

RESULT 38

ADE76651 ID ADE76651 standard; protein; 313 AA.  
XX AC ADE76651;  
XX DT 29-JUN-2004 (first entry)

XX Human thymidylate synthase mutant enzyme 12.  
XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell; KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant; KW mutant; 5-Fluorouridine; 5-FdUR.

XX OS Synthetic.  
OS Homo Sapiens.

XX Key Location/Qualifiers  
FT Misc-difference 254  
FT /note= "Wild-type Asp replaced by Glu"  
XX PN EP1316604-A1.  
XX PD 04-JUN-2003.  
XX PR 29-JUN-2002; 2002EP-00014489.  
XX PA (GEUR/) GEURTSEN W.  
XX PI Loeb L, Geurtzen W;  
XX DR WPI; 2003-495241/47.  
XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors.

XX New thymidylate synthase mutant, useful for protecting normal cell  
 PT populations against toxicity from thymidylate synthase inhibitors, or  
 PT differs from human wild-type thymidylate synthase in single, double, or  
 PT multiple mutations.  
 XX

Claim 2; Page: 36pp; English.

CC This invention relates to a novel thymidylate synthase mutant that  
 CC differs from human wild-type thymidylate synthase by one, two or more  
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a  
 CC result interfere with the DNA-metabolism of tumour cells. The protein  
 CC mutant is useful for the transfection of human cells which may be  
 CC affected by side effects due to chemotherapy with thymidylate synthase  
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,  
 CC or for transfection of early progenitor cells separated or grown from  
 CC bone marrow cells. The protein mutant is also used for identifying new  
 CC nucleotide analogues that inhibit normal human thymidylate synthase, or for  
 CC protecting human cell populations, preferably mucosa, against the toxic  
 CC manifestation of analogues that inhibit thymidylate synthase, or for  
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions  
 CC for the protection of human mucosa against ulceration under chemotherapy  
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the  
 CC mutant protein of the invention can also be used in gene therapy. The  
 CC present sequence is that of a mutant human thymidylate synthase (TS)  
 CC enzyme of the invention which displayed resistance to the TS-inhibitor  
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the  
 CC specification but was created by the indexer from information given in  
 CC the claims and the wild-type human TS sequence.  
 XX

SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;

Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198

RESULT 39  
 ADE76631 ID ADE76631 standard; protein; 313 AA.  
 XX AC ADE76631;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human thymidylate synthase mutant enzyme 6.  
 XX FH thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 KW muttein; 5-Fluorouridine; 5-FdUR.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 116 /note= "Wild-type Asp replaced by Ala"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PF 29-JUN-2002; 2002EP-00014489.  
 XX PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSEN W.  
 XX

RESULT 40  
 ADE76627 ID ADE76627 standard; protein; 313 AA.  
 XX AC ADE76627;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human thymidylate synthase mutant enzyme 2.  
 XX FH thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
 KW muttein; 5-Fluorouridine; 5-FdUR.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 53 /note= "Wild-type Thr replaced by Ser"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PF 29-JUN-2002; 2002EP-00014489.  
 XX PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSEN W.  
 XX

XX (GEUR/) GEURTSSEN W.  
 PA XX  
 PI Loeb L, Geurtseen W;  
 XX DR WPI; 2003-495241/47.  
 XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 XX PS Claim 2; Page: 36pp; English.

CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX Sequence 313 AA;  
 SQ Score 100.0%; Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; N mismatches 0; Indels 0; Gaps 0;  
 Query Match 100.0%; Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

XX PT 29-JAN-2004 (first entry)  
 DE Human thymidylate synthase mutant enzyme 5.  
 XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; chemotherapy; thymidylate synthase inhibitor; early progenitor cell; cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant; mutine; 5-fluorouridine; 5-FdUR.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 PH Location/Qualifiers  
 PT Misc-difference 110 /note= "Wild-type Asp replaced by Glu"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PN EP1316604-A1.

XX PF 29-JUN-2002; 2002EP-00014489.  
 XX PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSSEN W.  
 XX PI Loeb L, Geurtseen W;  
 XX XX WPI; 2003-495241/47.  
 XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 XX PS Claim 2; Page: 36pp; English.

CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, or for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX Sequence 313 AA;  
 SQ Score 100.0%; Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; N mismatches 0; Indels 0; Gaps 0;  
 Query Match 100.0%; Score 56; DB 7; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

XX AC ADE76630;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human thymidylate synthase mutant enzyme 14.  
 XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; chemotherapy; thymidylate synthase inhibitor; early progenitor cell; cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant; mutine; 5-fluorouridine; 5-FdUR.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 PH Location/Qualifiers  
 PT Misc-difference 254 /note= "Wild-type Asp replaced by Asn"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PN EP1316604-A1.

XX Key Location/Qualifiers  
 PT Misc-difference 254 /note= "Wild-type Asp replaced by Asn"  
 XX PN EP1316604-A1.

XX Key Location/Qualifiers  
 PT Misc-difference 254 /note= "Wild-type Asp replaced by Asn"  
 XX PN EP1316604-A1.

XX 04-JUN-2003. /note= "Wild-type Phe replaced by Ser"

PD XX FT Misc-difference 169  
XX FT Misc-difference 254 /note= "Wild-type Lys replaced by Arg"

PP 29-JUN-2002; 2002EP-00014489.  
XX FT Misc-difference 254 /note= "Wild-type Asp replaced by Glu"

PR 03-DEC-2001; 2001US-0334557P.  
XX PN EP1316604-A1.

PA XX PD 04-JUN-2003.  
PI XX PP 29-JUN-2002; 2002EP-00014489.  
DR XX PR 03-DEC-2001; 2001US-0334557P.

XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, or differs from human wildtype thymidylate synthase in single, double or multiple mutations.

PT XX PA (GEUR/) GEURTSEN W.  
PI XX PI Loeb L, Geurtzen W;  
WPI; 2003-495241/47.

XX PR New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, or differs from human wildtype thymidylate synthase in single, double or multiple mutations.

XX PS Claim 2; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 IMALPPCHAL 198

Qy 1 IMALPPCHAL 10  
Db 189 IMALPPCHAL 198

Query Match 100.0%; Score 56; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IMALPPCHAL 10  
Db 189 IMALPPCHAL 198

RESULT 44  
ADE76641 ID ADE76641 standard; protein; 313 AA.  
XX AC ADE76641;  
XX DT 29-JAN-2004 (first entry)  
DB Human thymidylate synthase mutant enzyme 27.

RESLT 43  
ADE76652 ID ADE76652 standard; protein; 313 AA.  
XX AC ADE76652;  
XX DT 29-JAN-2004 (first entry)  
DB Human thymidylate synthase mutant enzyme 16.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;  
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;  
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;  
KW muttein; 5-Fluorouridine; 5-FdUR.  
XX OS Homo sapiens.  
XX Key-Location/Qualifiers  
PT Misc-difference 117

KW mutein; 5-fluorouridine; 5-FdUR.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FT Misc-difference 258  
 FT /note= "Wild-type Tyr replaced by Phe"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PP 29-JUN-2002; 2002EP-00014489.  
 PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSEN W.  
 PI Loeb L, Geurtzen W;  
 XX DR 2003-495241/47.  
 XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 PT  
 PT  
 PT  
 PT  
 XX PS Claim 2 ; Page: 36pp; English.  
 XX This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX SQ Sequence 313 AA;  
 Query Match Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198  
 RESULT 45  
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 XX AC ADE76644;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human thymidylate synthase mutant enzyme 19.  
 XX ID ADE76656 standard; protein; 313 AA.

KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell; KW cytotoxic; human mucosa ulceration; gene therapy; human; enzyme; mutant; KW mutein; 5-fluorouridine; 5-FdUR.  
 XX  
 Key Location/Qualifiers  
 FT Misc-difference 5  
 FT /note= "Wild-type Gly replaced by Ser"  
 FT Misc-difference 78  
 FT /note= "Wild-type Arg replaced by Cys"  
 FT Misc-difference 219  
 FT /note= "Wild-type Met replaced by Ile"  
 XX PN EP1316604-A1.  
 XX PD 04-JUN-2003.  
 XX PP 29-JUN-2002; 2002EP-00014489.  
 XX PR 03-DEC-2001; 2001US-0334557P.  
 XX PA (GEUR/) GEURTSEN W.  
 PI Loeb L, Geurtzen W;  
 XX DR 2003-495241/47.  
 XX PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.  
 XX PS Claim 4 ; Page: 36pp; English.  
 XX This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.  
 XX SQ Sequence 313 AA;  
 Query Match Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198  
 RESULT 46  
 ADE76656 ID ADE76656 standard; protein; 313 AA.  
 XX AC ADE76656;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human thymidylate synthase mutant enzyme 19.  
 XX ID ADE76656 standard; protein; 313 AA.

Query Match Score 56; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LMALPPCHAL 10  
 Db 189 LMALPPCHAL 198  
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 ADE76656 ID ADE76656 standard; protein; 313 AA.



Query Match	100.0%	Score 56;	DB 7;	Length 313;			
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Db	189 LMALPPCHAL 198						
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ID ADE76625	standard; protein; 313 AA.						
XX DT 29-JAN-2004 (first entry)							
XX AC ADE76625;							
XX ID ADE76625							
XX DB Human thymidylate synthase wild-type sequence.							
XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell; cytotoxicity; thymidylate synthase inhibitor; early progenitor cell; human mucosa ulceration; gene therapy; human; enzyme; mutant; mutagen; 5-fluorouridine; 5-FdUR.							
XX OS Homo sapiens.							
XX PN EP1316604-A1.							
XX XX							
XX PD 04-JUN-2003.							
XX XX							
XX PF 29-JUN-2002; 2002EP-00014489.							
XX XX							
PR 03-DEC-2001; 2001US-0334557P.							
XX XX							
PA (GEUR/) GEURTSEN W.							
XX PI Loeb L, Geurtzen W;							
XX XX							
DR WPI; 2003-495241/47.							
XX XX							
PT New thymidylate synthase mutant, useful for protecting normal cell populations against toxicity from thymidylate synthase inhibitors, differs from human wildtype thymidylate synthase in single, double or multiple mutations.							
XX PS Disclosure; Fig 2; 36pp; English.							
XX CC This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cell. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.							
XX SQ Sequence 313 AA;							
Query Match	100.0% ;	Score 56;	DB 7;	Length 313;			
Best Local Similarity	100.0% ;	Pred. No. 0.55;					
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
SQ	1 LMALPPCHAL 10						
Query Match	100.0% ;	Score 56;	DB 7;	Length 313;			
Best Local Similarity	100.0% ;	Pred. No. 0.55;					
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			



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## OM protein - protein search, using SW model

Run on: February 17, 2006, 02:45:36 ; Search time 17 seconds  
 8.362 Million cell updates/sec

Title: US-10-734-049B-188

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 Sequence: 1 LMAPPCHAL 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	52	92.9	257	6	US-10-467-2358	Sequence 2358, AP
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3	40	71.4	264	7	US-11-167-067A-28	Sequence 28, AP
4	40	71.4	264	7	US-11-167-067B-45	Sequence 45, AP
5	36	64.3	111	7	US-11-184-005-5	Sequence 5, AP
6	35	62.5	232	6	US-10-822-234-1023	Sequence 1023, AP
7	33	60.7	111	7	US-11-072-512-2358	Sequence 2358, AP
8	33	58.9	23	7	US-11-058-783-112	Sequence 112, AP
9	33	58.9	271	6	US-10-352-783-52	Sequence 52, AP
10	33	58.9	296	7	US-11-162-041-233	Sequence 233, AP
11	33	58.9	688	7	US-11-131-035-2	Sequence 2, AP
12	33	58.9	1042	7	US-11-067-111-1	Sequence 1, AP
13	33	58.9	1047	7	US-11-124-367A-388	Sequence 388, AP
14	33	58.9	1058	7	US-11-124-367A-386	Sequence 386, AP
15	33	58.9	1062	7	US-11-124-367A-387	Sequence 387, AP
16	32	57.1	106	7	US-11-072-512-2662	Sequence 2662, AP
17	32	57.1	145	7	US-11-072-512-2271	Sequence 2271, AP
18	32	57.1	191	6	US-10-995-561-824	Sequence 824, AP
19	32	57.1	236	6	US-10-995-561-823	Sequence 823, AP
20	32	57.1	236	6	US-10-523-038-5	Sequence 5, AP
21	32	57.1	237	6	US-10-523-038-45	Sequence 45, AP
22	32	57.1	328	6	US-10-131-826-34	Sequence 34, AP
23	32	57.1	391	6	US-10-995-561-892	Sequence 892, AP
24	32	57.1	391	6	US-10-995-561-893	Sequence 893, AP
25	32	57.1	400	7	US-11-169-041-158	Sequence 158, AP

99	6	US-10-770-726-45	Sequence 45, App1	Sequence 27, App1
100	7	US-11-235-732-2	Sequence 2, App1	Sequence 179, App
101	30	53.6	3095	7 US-11-235-732-4
102	30	53.6	3100	7 US-11-235-732-7
103	30	53.6	3567	6 US-10-453-372-1112
104	29	51.8	111	7 US-11-195-197-10
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106	29	51.8	12	6 US-10-511-314-1
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132	29	51.8	306	7 US-11-017-550-45
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136	29	51.8	369	7 US-11-105-288-60
137	29	51.8	381	6 US-11-052-550-58
138	29	51.8	444	7 US-11-052-550A-67
139	29	51.8	481	7 US-11-072-512-2394
140	29	51.8	492	7 US-11-072-512-2254
141	29	51.8	514	7 US-11-195-739-1
142	29	51.8	531	6 US-10-453-372-132
143	29	51.8	538	6 US-10-453-372-132
144	29	51.8	540	6 US-10-512-234-1395
145	29	51.8	560	6 US-10-163-712A-79
146	29	51.8	568	7 US-11-093-666-10588
147	29	51.8	580	6 US-10-453-372-138
148	29	51.8	580	6 US-10-453-372-144
149	29	51.8	585	7 US-11-127-877-63
150	29	51.8	638	6 US-10-453-372-166
151	29	51.8	761	6 US-10-453-372-126
152	29	51.8	823	6 US-10-453-372-124
153	29	51.8	826	6 US-10-453-372-124
154	29	51.8	826	6 US-10-453-372-118
155	29	51.8	826	6 US-10-453-372-156
156	29	51.8	826	6 US-10-453-372-166
157	29	51.8	826	6 US-10-453-372-172
158	29	51.8	826	6 US-11-453-372-174
159	29	51.8	823	6 US-10-453-372-176
160	29	51.8	832	6 US-10-453-372-120
161	29	51.8	832	6 US-11-227-877-74
162	29	51.8	1062	6 US-10-453-372-1079
163	29	51.8	1085	6 US-10-523-477-13
164	29	51.8	1087	7 US-11-117-169-10
165	29	51.8	1115	7 US-10-932-23B-60
166	29	51.8	1481	7 US-11-072-386-30
167	29	51.8	1733	7 US-11-182-016-21
168	29	51.8	1798	6 US-10-995-561-1033
169	29	51.8	1798	6 US-10-980-991-96
170	29	51.8	1960	7 US-11-149-003-16
171	29	51.8	1960	7 US-11-077-386-29
172	29	51.8	2061	7 US-11-169-041-179
173	29	51.8	2061	7 US-10-453-372-170
174	29	51.8	2061	7 US-10-453-372-114
175	29	51.8	2061	7 US-10-453-372-148
176	29	51.8	2061	7 US-10-453-372-136
177	29	51.8	2061	7 US-10-453-372-142
178	29	51.8	2061	7 US-10-453-372-146
179	29	51.8	2061	7 US-10-453-372-146
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181	29	51.8	2061	7 US-10-453-372-154
182	29	51.8	2061	7 US-10-453-372-168
183	29	51.8	2061	7 US-10-453-372-116
184	29	51.8	2061	7 US-10-922-232B-16
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192	28	50.0	2061	16 US-11-072-512-295
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223	28	50.0	2061	16 US-11-184-574-4
224	28	50.0	2061	16 US-09-978-360A-110
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246	28	50.0	1477	7	US-11-149-003-8	Sequence 8, App1	540	App
247	28	50.0	1512	7	US-11-149-003-10	Sequence 10, App1	59	App1
248	28	50.0	1535	7	US-11-149-003-14	Sequence 14, App1	155	App
249	28	50.0	1538	6	US-10-329-258-14	Sequence 14, App1	649	3
250	28	50.0	1570	7	US-11-149-003-12	Sequence 12, App1	156	1
251	28	50.0	1593	7	US-11-149-003-4	Sequence 4, App1	869	12
252	28	50.0	1628	7	US-11-149-003-2	Sequence 2, App1	869	16
253	28	50.0	1637	6	US-10-822-234-1204	Sequence 1204, App1	899	App
254	28	50.0	2050	6	US-10-453-372-192	Sequence 192, App	2420	App
255	28	50.0	2280	7	US-11-022-562-211	Sequence 211, App	2	App1
256	28	50.0	3714	6	US-10-994-561-1016	Sequence 2, App1	394	App
264	28	50.0	3717	6	US-10-821-234-1076	Sequence 1015, App1	6	App1
265	27	49.1	261	6	US-10-822-234-930	Sequence 1076, App1	2	App1
266	27	49.1	273	5	US-09-978-360A-709	Sequence 10, App1	319	App1
267	27	48.2	50	7	US-11-004-463-919	Sequence 6, App1	320	App
268	27	48.2	51	6	US-10-467-657-1244	Sequence 1016, App1	321	App
269	27	48.2	58	6	US-10-467-657-3262	Sequence 1015, AD	322	App
270	27	48.2	58	6	US-10-467-657-6856	Sequence 1016, AD	323	App
271	27	48.2	101	7	US-11-072-512-2117	Sequence 930, App1	324	App
272	27	48.2	104	7	US-11-072-512-2466	Sequence 919, App1	325	App
273	27	48.2	105	6	US-10-986-501-112	Sequence 124, App1	326	App
274	27	48.2	105	6	US-10-821-234-1149	Sequence 3262, App1	327	App
275	27	48.2	106	6	US-10-821-234-1191	Sequence 6856, App1	328	App
276	27	48.2	106	7	US-11-072-512-1964	Sequence 2117, AD	329	App
277	27	48.2	112	6	US-10-678-790-62	Sequence 2466, App1	330	App
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280	27	48.2	127	7	US-11-072-512-2861	Sequence 2861, App1	333	App
281	27	48.2	127	7	US-11-072-512-3075	Sequence 1191, App1	334	App
282	27	48.2	148	7	US-11-147-047-30	Sequence 3075, App1	335	App
283	27	48.2	155	7	US-11-072-512-3331	Sequence 30, App1	336	App
284	27	48.2	158	7	US-11-072-512-3610	Sequence 331, App1	337	App
285	27	48.2	159	7	US-11-147-047-29	Sequence 3610, App1	338	App
286	27	48.2	173	6	US-10-821-234-1291	Sequence 29, App1	339	App
287	27	48.2	201	7	US-11-057-012-4	Sequence 1291, App1	340	App
288	27	48.2	203	7	US-11-155-141-4	Sequence 4, App1	341	App
289	27	48.2	205	6	US-10-659-742-72	Sequence 72, App1	342	App
290	27	48.2	211	7	US-11-058-662-16	Sequence 16, App1	343	App
291	27	48.2	211	7	US-11-155-141-21	Sequence 21, App1	344	App
292	27	48.2	211	7	US-11-072-512-3219	Sequence 3219, App1	345	App
293	27	48.2	213	7	US-11-072-512-2657	Sequence 2657, App1	346	App
294	27	48.2	216	7	US-11-072-512-3032	Sequence 3032, App1	347	App
295	27	48.2	229	6	US-10-131-822A-178	Sequence 178, App1	348	App
296	27	48.2	269	6	US-10-467-657-916	Sequence 916, App1	349	App
297	27	48.2	273	6	US-11-098-686-10888	Sequence 1088, A	350	App
303	27	48.2	275	6	US-10-532-477-10	Sequence 10, App1	351	App
304	27	48.2	299	6	US-10-967-671-13	Sequence 13, App1	352	App
305	27	48.2	306	7	US-11-019-711-90	Sequence 90, App1	353	App
306	27	48.2	307	7	US-11-019-711-91	Sequence 10367, A	354	App
307	27	48.2	312	7	US-11-197-721-14	Sequence 1143, A	355	App
308	27	48.2	333	6	US-10-980-234-1684	Sequence 1684, App1	356	App
310	27	48.2	333	6	US-10-980-388-114	Sequence 1088, A	357	App
311	27	48.2	333	7	US-11-050-440-2	Sequence 2, App1	358	App
312	27	48.2	336	7	US-11-197-721-10	Sequence 10, App1	359	App
313	27	48.2	342	7	US-11-072-512-2201	Sequence 2201, App1	360	App
314	27	48.2	353	7	US-11-058-686-10774	Sequence 1074, A	361	App
315	27	48.2	358	6	US-10-770-726-60	Sequence 60, App1	362	App
316	27	48.2	363	6	US-10-955-561-541	Sequence 541, App1	363	App
317	27	48.2	374	7	US-11-057-012-51	Sequence 51, App1	364	App

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393	27	48.2	1519	7	US-11-182-016-5	Sequence 5, App1	465	6	US-10-995-561-685
394	27	48.2	1730	7	US-11-182-016-19	Sequence 19, App1	466	6	US-10-995-561-686
395	27	48.2	1907	7	US-11-039-338-25	Sequence 25, App1	467	6	US-10-995-561-687
396	27	48.2	2011	7	US-11-080-991-56	Sequence 56, App1	468	6	US-11-186-384-43
397	27	48.2	2353	7	US-11-037-243-64	Sequence 64, App1	469	6	US-11-185-877-11
398	27	48.2	2635	7	US-11-019-711-47	Sequence 47, App1	470	6	US-11-080-091-4
399	27	48.2	3748	7	US-11-132-616-8	Sequence 8, App1	471	6	US-11-080-914-4
400	27	48.2	3749	7	US-11-132-616-6	Sequence 6, App1	472	6	US-10-821-234-923
401	27	48.2	3749	7	US-11-132-616-12	Sequence 19, App1	473	7	US-11-087-177-19
402	27	48.2	3912	7	US-11-132-616-5	Sequence 12, App1	474	6	US-11-087-177-21
403	27	48.2	3913	7	US-11-132-616-7	Sequence 7, App1	475	7	US-10-131-526A-96
404	27	48.2	3913	7	US-11-132-616-9	Sequence 5, App1	476	7	US-11-012-162-50
405	26	46.5	47.3	72	US-10-167-657-1502	Sequence 9, App1	477	6	US-11-120-108-188
406	26	46.5	529	7	US-11-122-144-2	Sequence 1502, App1	478	6	US-11-122-762-62
407	26	46.4	14	7	US-11-093-724B-16	Sequence 2, App1	479	6	US-11-080-091-12
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409	26	46.4	26	48	US-11-123-896-303	Sequence 12, App1	481	7	US-10-793-526-1428
410	26	46.4	26	48	US-10-167-657-3928	Sequence 1, App1	482	6	US-11-012-222-7
411	26	46.4	57	6	US-10-467-657-3928	Sequence 303, App1	483	6	US-10-525-674-42
412	26	46.4	64	7	US-11-123-896-117	Sequence 3928, App1	483	6	US-11-120-108-188
413	26	46.4	75	7	US-11-123-896-116	Sequence 1502, App1	484	6	US-11-122-762-62
414	26	46.4	75	7	US-11-123-896-119	Sequence 11, App1	485	6	US-10-93-099-68
415	26	46.4	75	7	US-11-123-896-302	Sequence 116, App1	486	6	US-11-107-512-3445
416	26	46.4	82	7	US-11-000-453-743	Sequence 11, App1	487	7	US-10-793-526-1428
417	26	46.4	82	7	US-11-000-453-744	Sequence 117, App1	488	7	US-11-122-222-7
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439	26	46.4	200	6	US-10-167-657-5256	Sequence 453, App1	510	6	US-10-989-142-8
440	26	46.4	202	6	US-10-167-657-5256	Sequence 454, App1	511	6	US-10-989-142-8
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448	26	46.4	255	7	US-11-196-067-2	Sequence 186, App1	519	6	US-10-989-142-8
449	26	46.4	264	7	US-11-128-512-2520	Sequence 72, App1	520	6	US-10-989-142-8
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451	26	46.4	219	6	US-10-167-657-5256	Sequence 152, App1	522	6	US-10-989-142-8
452	26	46.4	232	7	US-11-128-505-66	Sequence 66, App1	523	6	US-10-989-142-8
453	26	46.4	244	6	US-10-167-657-5648	Sequence 2792, App1	524	6	US-10-989-142-8
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456	26	46.4	315	6	US-11-053-312-212	Sequence 6, App1	527	6	US-10-989-142-8
457	26	46.4	329	7	US-11-080-686-10153	Sequence 95, App1	528	6	US-10-989-142-8
458	26	46.4	332	6	US-10-131-826A-386	Sequence 10153, A	529	6	US-10-989-142-8
459	26	46.4	337	6	US-10-080-388-115	Sequence 115, App1	530	6	US-10-989-142-8
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463	26	46.4	339	6	US-10-995-561-681	Sequence 681, App1	534	6	US-10-989-142-8

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550	6	US-10-495-662-20	Sequence 20, App
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ALIGNMENTS

**RESULT 1**  
USPTO 10-467-657-2358  
Sequence 2358, Application US10467657  
Publication No. US20050260581A1  
**GENERAL INFORMATION:**  
APPLICANT: CHIRON SpA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
**TITLE OF INVENTION:** GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

APPLICANT: Haberhauer, Gregor  
 TITLE OF INVENTION: CORINOBACTERIUM GLUTAMICUM GENES ENCODING  
 TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
 FILE REFERENCE: BGI-12-CPCN  
 CURRENT APPLICATION NUMBER: US/11/055, 822  
 CURRENT FILING DATE: 2005-02-11  
 PRIOR APPLICATION NUMBER: 09/606, 740  
 PRIOR FILING DATE: 2000-06-23  
 PRIOR APPLICATION NUMBER: 60/141, 031  
 PRIOR FILING DATE: 1999-06-25  
 PRIOR APPLICATION NUMBER: 60/142, 101  
 PRIOR FILING DATE: 1999-07-02  
 PRIOR APPLICATION NUMBER: 60/148, 613  
 PRIOR FILING DATE: 1999-08-12  
 PRIOR APPLICATION NUMBER: 60/187, 970  
 PRIOR FILING DATE: 2000-03-09  
 PRIOR APPLICATION NUMBER: DE 19930476.9  
 PRIOR FILING DATE: 1999-07-01  
 PRIOR APPLICATION NUMBER: DE 19931415.2  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931418.7  
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 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: DE 19931420.9  
 PRIOR FILING DATE: 1999-07-08  
 Remaining Prior Application data removed - See File Wrapper or  
 NUMBER OF SEQ ID NOS: 1158

RESULT 3  
US-11-165-067A-28  
; Sequence 28, Application US/11165067A  
; Publication No. US20060014257A1  
; GENERAL INFORMATION:  
; APPLICANT: KATASHKINA Joanna Yosifovna  
; APPLICANT: SKOROKHODOVA Aleksandra Yurievna  
; APPLICANT: ZIMENKOV Daniil Vadimovich  
; APPLICANT: GULEVICH Andrey Yurievich  
; APPLICANT: ERASAS Lopes Lubo  
; APPLICANT: BIRYUKOVA Irina Vladimirovna  
; APPLICANT: MIRONOV Aleksandr Sergeevich  
; APPLICANT: MASHKO Sergey Vladimirovich  
; TITLE OF INVENTION: RSF1010 DERIVATIVE Mob- PLASMID CONTAINING NO ANTIBIOTIC  
; TITLE OF INVENTION: BACTERIUM COMPRISING THE VECTOR AND METHOD FOR PRODUC-  
; FILE REFERENCE: US-174  
; CURRENT APPLICATION NUMBER: US/11/165,067A  
; CURRENT FILING DATE: 2005-06-24  
; PRIORITY APPLICATION NUMBER: RU2004119027  
; PRIOR FILING DATE: 2004-06-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.1  
; SEO ID NO: 28

TYP: PRT ORGANISM: Escherichia coli  
3-11-165-067A-28

Query Match	Score	DB	Length
Boot Local Similarity	71.4% 87 5%	No 3 7.	264;

**RESULT 4**  
US-11-165-067A-45  
Sequence 45, Application US/11165067A  
Publication No. US200600425741  
GENERAL INFORMATION:  
APPLICANT: KATASHKINA Joanna Yosifovna  
APPLICANT: SKOROKHOVA Aleksandra Yurievna  
APPLICANT: ZIMENKOVA Danila Vadimovich  
APPLICANT: GULEVICH Andrey Yurievich  
APPLICANT: BIRRAIS Lopes Lubov  
APPLICANT: MIRONOV Aleksandr Sergeevich  
APPLICANT: MASHKO Sergei Vladimirovich  
TITLE OF INVENTION: RSP1010 DIBRIVATIVE Mob- PLASMID CONTAINING NO ANTIOTIC RESISTANT  
FILE REFERENCE: US-174  
CURRENT APPLICATION NUMBER: US/11/165-067A  
FILE FILING DATE: 2005-06-24  
PRIORITY NUMBER: RU2004119027  
NUMBER OF SEQ ID NOS: 48  
SEQ ID NO: 45  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Escherichia coli  
PRIORITY FILING DATE: 2004-06-24  
PRIORITY NUMBER: RU2004119027  
NUMBER OF SEQ ID NOS: 48  
SEQ ID NO: 45  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-11-165-067A-45

Query Match Score 40; DB 7; Length 264;  
Best Local Similarity 87.5%; Pred. No. 3.7%;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCRA 9  
Db 141 MALAPCRA 148

**RESULT 5**  
US-11-184-005-5  
Sequence 5, Application US/11184005  
Publication No. US2005025605241  
GENERAL INFORMATION:  
APPLICANT: Layten, Frank P.  
APPLICANT: Moos, Malcolm J.R.  
APPLICANT: Hoang, Bang  
APPLICANT: Wang, Shouwen  
TITLE OF INVENTION: METHOD OF MODULATING TISSUE  
TITLE OF INVENTION: NIFH133\_1CPC3  
FILE REFERENCE: NIFH133\_1CPC3  
CURRENT APPLICATION NUMBER: US/11/184.005  
CURRENT FILING DATE: 2005-07-18  
PRIORITY NUMBER: US 10/028051  
PRIOR FILING DATE: 2001-12-19  
PRIORITY NUMBER: US 08/822333  
PRIOR FILING DATE: 1997-03-20  
PRIORITY NUMBER: US 08/729,452  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 5  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
us-11-184-005-5

Query Match Score 36; DB 7; Length 111;

**RESULT 6**  
US-10-821-234-1023  
Sequence 1023, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmani, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIORITY NUMBER: US 60/462,047  
PRIORITY FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt\_SEQ\_Genes Version 1.0  
SEQ ID NO: 1023  
LENGTH: 232  
TYPE: PRT  
ORGANISM: Homo sapiens  
us-10-821-234-1023

Query Match Score 35; DB 6; Length 232;  
Best Local Similarity 60.0%;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IMALPPCHAL 10  
Db 52 LLPPCCRAL 61

**RESULT 7**  
US-11-072-512-2358  
Sequence 2358, Application US/11072512  
Publication No. US20060029945A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: TRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOKIKO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIORITY NUMBER: US 60/350,978  
PRIORITY NUMBER: JP 2001-3179298  
PRIORITY NUMBER: JP 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2358  
; LENGTH: 111  
; ORGANISM: Homo sapiens  
US-11-072-512-2358

Query Match Score 34; DB 7; Length 111;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PPCHAL 10  
Db 90 PPCHRL 95

RESULT 8  
US-11-068-783-112  
; Sequence 112, Application US/11068783  
; Publication No. US2005026075A1  
; GENERAL INFORMATION:  
; APPLICANT: Burian, Jan  
; BARTFIELD, Daniel  
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING  
; ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS  
; FILE REFERENCE: 660081.411  
; CURRENT APPLICATION NUMBER: US/11/068,783  
; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/09/444,281  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 112  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Trimeresurus wagleri

US-11-068-783-112  
Query Match Score 33; DB 7; Length 23;  
Best Local Similarity 80.0%; Pred. No. 6;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LPPCH 8  
Db 11 IPPCH 15

RESULT 9  
US-10-353-783-52  
; Sequence 52, Application US/10353783  
; Publication No. US20050261175A1  
; GENERAL INFORMATION:  
; APPLICANT: Zeebo, Krisztina M.  
; Boselman, Robert A.  
; Suggs, Sidney V.  
; Martin, Francis H.  
; TITLE OF INVENTION: Stem Cell Factor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0., Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/353,783  
; FILING DATE: 28-Jan-2003  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/448,729  
FILING DATE: 24-MAY-1995  
APPLICATION NUMBER: 08/172,329  
FILING DATE: 21-DEC-1993  
APPLICATION NUMBER: 07/942,255  
FILING DATE: 26-NOV-1992  
APPLICATION NUMBER: 07/694,535  
FILING DATE: 10-APR-1991  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/32958A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: <Unknown>  
TELEFAX: 312/474-6300  
TELEX: 311/4-0448  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 271 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-10-353-783-52

Query Match 58.9%; Score 33; DB 6; Length 271;  
Best Local Similarity 60.0%; Pred. No. 59;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10  
Db 215 VMALLPACFSL 224

RESULT 10  
US-11-169-041-233  
; Sequence 233, Application US/11169041  
; Publication No. US20060019284A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 1001 NP  
; CURRENT APPLICATION NUMBER: US/11/169,041  
; CURRENT FILING DATE: 2005-06-28  
; PRIOR APPLICATION NUMBER: 60/584,405  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 527  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-169-041-233  
Query Match 58.9%; Score 33; DB 7; Length 296;  
Best Local Similarity 71.4%; Pred. No. 64;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCH 8  
:|||

```

Db    88 LALAPCH 94
      ; CURRENT APPLICATION NUMBER: US/11/124,367A
      ; CURRENT FILING DATE: 2005-05-09
      ; PRIORITY APPLICATION NUMBER: US 60/568,846
      ; PRIORITY FILING DATE: 2004-05-07
      ; PRIORITY APPLICATION NUMBER: US 60/582,609
      ; PRIORITY FILING DATE: 2004-06-25
      ; PRIORITY APPLICATION NUMBER: US 60/599,554
      ; PRIORITY FILING DATE: 2004-08-09
      ; NUMBER OF SEQ ID NOS: 34460
      ; SOFTWARE: FastSEQ for Windows Version 4.0
      ; SEQ ID NO: 388
      ; LENGTH: 1047
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-11-124-367A-388

      Query Match      58.9%; Score 33; DB 7; Length 1047;
      Best Local Similarity 72.7%; Pred. No. 2.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
      Qy   1 LMALPP--CHA 9
      Db   118 LMALPTTICHA 128

      RESULT 14
      ; Sequence 386, Application US/11124367A
      ; Publication No. US20060024700A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Michele Cargill
      ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
      ; Fibrosis Methods of Detection and Uses Thereof
      ; FILE REFERENCE: CL001519.ORD
      ; CURRENT APPLICATION NUMBER: US/11/124,367A
      ; CURRENT FILING DATE: 2005-05-09
      ; PRIORITY APPLICATION NUMBER: US 60/568,846
      ; PRIORITY FILING DATE: 2004-05-07
      ; PRIORITY APPLICATION NUMBER: US 60/582,609
      ; PRIORITY FILING DATE: 2004-06-25
      ; PRIORITY APPLICATION NUMBER: US 60/599,554
      ; PRIORITY FILING DATE: 2004-08-09
      ; NUMBER OF SEQ ID NOS: 34460
      ; SOFTWARE: FastSEQ for Windows Version 4.0
      ; SEQ ID NO: 386
      ; LENGTH: 1058
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-11-124-367A-386

      Query Match      58.9%; Score 33; DB 7; Length 1058;
      Best Local Similarity 72.7%; Pred. No. 2.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
      Qy   1 LMALPP--CHA 9
      Db   129 LMALPTTICHA 139

      RESULT 15
      ; Sequence 387, Application US/11124367A
      ; Publication No. US20060024700A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Michele Cargill
      ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
      ; Fibrosis Methods of Detection and Uses Thereof
      ; FILE REFERENCE: CL001519.ORD
      ; CURRENT APPLICATION NUMBER: US/11/124,367A
      ; CURRENT FILING DATE: 2005-05-09
      ; PRIORITY APPLICATION NUMBER: US 60/568,846

      RESULT 16
      ; Sequence 388, Application US/11124367A
      ; Publication No. US20060024700A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Michele Cargill
      ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
      ; Fibrosis Methods of Detection and Uses Thereof
      ; FILE REFERENCE: CL001519.ORD
      ; CURRENT APPLICATION NUMBER: US/11/124,367A
      ; CURRENT FILING DATE: 2005-05-09
      ; PRIORITY APPLICATION NUMBER: US 60/568,846

```

PRIOR FILING DATE: 2004-05-07  
 PRIOR APPLICATION NUMBER: US 60/582,609  
 PRIOR FILING DATE: 2004-06-25  
 PRIOR APPLICATION NUMBER: US 60/599,554  
 PRIOR FILING DATE: 2004-08-09  
 NUMBER OF SEQ ID NOS: 34460  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 387  
 LENGTH: 1062  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 us-11-124-367A-387

Query Match Score 58.9%; DB 7; Length 1062;  
 Best Local Similarity 72.7%; Pred. No. 2.1e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy	1 LMALPP--CHA 9
Db	133 LMALPTTCHAA 143

RESULT 16  
 US-11-072-512-2662  
 Sequence 2662, Application US/11072512  
 Publication No. US20060029945A1  
 GENERAL INFORMATION:  
 APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKI, ICHIRO  
 APPLICANT: SEKI, NAOKI  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: OTSUKA, MOTOKI  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: MASTHO, YASUHIKO  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT APPLICATION NUMBER: US/11/072,512  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US 60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298  
 PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2271  
 LENGTH: 145  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-072-512-2271

RESULT 17  
 US-11-072-512-2662  
 Sequence 2662, Application US/11072512  
 Publication No. US20060029945A1  
 GENERAL INFORMATION:  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF NUMBER OF SEQ ID NOS: 4096  
 FILE REFERENCE: CL001559  
 CURRENT APPLICATION NUMBER: US/10/995,561  
 CURRENT FILING DATE: 2004-11-24  
 NUMBER OF SEQ ID NOS: 85702  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 824  
 LENGTH: 191  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-995-561-824

Query Match Score 57.1%; DB 7; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6 PCHAL 10
Db	58 PCHAL 62

RESULT 18  
 US-10-995-561-824  
 Sequence 824, Application US/10995561  
 Publication No. US20052722054A1  
 GENERAL INFORMATION:  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF NUMBER OF SEQ ID NOS: 4096  
 FILE REFERENCE: CL001559  
 CURRENT APPLICATION NUMBER: US/10/995,561  
 CURRENT FILING DATE: 2004-11-24  
 NUMBER OF SEQ ID NOS: 85702  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 824  
 LENGTH: 191  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-995-561-824

Query Match Score 57.1%; DB 6; Length 191;  
 Best Local Similarity 57.1%; Pred. No. 64;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LMALPPC 7
Db	141 ILSLPPC 147

RESULT 19  
 US-11-072-512-2271  
 Sequence 2271, Application US/11072512

RESULT 19  
 Sequence 823, Application US/10995561  
 Publication No. US200502720541  
 GENERAL INFORMATION  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF  
 CURRENT APPLICATION NUMBER: US/10/995,561  
 CURRENT FILING DATE: 2004-11-24  
 NUMBER OF SEQ ID NOS: 95702  
 SEQ ID NO: 823  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-995-561-823

Query Match Similarity 57.1% Score 32; DB 6; Length 236;  
 Best Local Similarity 57.1% Pred. No. 77;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Features:  
 1 IMLAPPC 7  
 Db 186 ILSLPPC 192

RESULT 20  
 Sequence 5, Application US/10523038  
 Publication No. US20050287649A1  
 GENERAL INFORMATION  
 APPLICANT: SMITH, Harold  
 APPLICANT: SOWDEN, Mark P.  
 APPLICANT: DEWHURST, Stephen  
 APPLICANT: WEDEKIND, Joseph  
 TITLE OF INVENTION: CHIMERIC PROTBINS RELATED COMPOUNDS, AND USES THEREOF  
 CURRENT APPLICATION NUMBER: US/10/523,038  
 CURRENT FILING DATE: 2005-02-02  
 NUMBER OF SEQ ID NOS: 49  
 SEQ ID NO: 5  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-523-038-5

Query Match Similarity 57.1% Score 32; DB 6; Length 237;  
 Best Local Similarity 57.1% Pred. No. 78;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Features:  
 1 IMLAPPC 7  
 Qy 187 ILSLPPC 193

RESULT 22  
 Sequence 34, Application US/10131826A  
 Publication No. US20050245730A1  
 GENERAL INFORMATION  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filivatoff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C128  
 CURRENT APPLICATION NUMBER: US/10/131,826A  
 CURRENT FILING DATE: 2002-04-24  
 PRIOR APPLICATION NUMBER: 60/049311  
 PRIOR FILING DATE: 1997-06-18  
 PRIOR APPLICATION NUMBER: 60/056974  
 PRIOR FILING DATE: 1997-08-16  
 PRIOR APPLICATION NUMBER: 60/059113  
 PRIOR FILING DATE: 1997-09-17  
 PRIOR APPLICATION NUMBER: 60/059115

Query Match Similarity 57.1% Score 32; DB 6; Length 236;  
 Best Local Similarity 57.1% Pred. No. 77;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Features:  
 1 IMLAPPC 7  
 Db 186 ILSLPPC 192

RESULT 21  
 Sequence 45, Application US/10523038  
 Publication No. US20050287649A1  
 GENERAL INFORMATION  
 APPLICANT: SMITH, Harold  
 APPLICANT: SOWDEN, Mark P.  
 APPLICANT: DEWHURST, Stephen  
 APPLICANT: KIM, Baek  
 APPLICANT: WEDEKIND, Joseph  
 TITLE OF INVENTION: PROTEIN TRANSDUCING DOMAIN/DEAMINASE  
 FILE REFERENCE: 21108.004U2  
 CURRENT APPLICATION NUMBER: US/10/523,038  
 CURRENT FILING DATE: 2005-02-02  
 PRIOR APPLICATION NUMBER: PCT/US03/24458  
 PRIOR FILING DATE: 2003-08-05  
 PRIOR APPLICATION NUMBER: 60/419,982  
 PRIOR FILING DATE: 2002-10-21  
 PRIOR APPLICATION NUMBER: 60/401,293  
 PRIOR FILING DATE: 2002-08-05  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 49  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-995-561-823

Query Match Similarity 57.1% Score 32; DB 6; Length 236;  
 Best Local Similarity 57.1% Pred. No. 78;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Features:  
 OTHER INFORMATION: Description of Artificial Sequence; note =  
 OTHER INFORMATION: synthetic construct  
 US-10-523-038-45

Query Match Similarity 57.1% Score 32; DB 6; Length 237;  
 Best Local Similarity 57.1% Pred. No. 78;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IMLAPPC 7  
 Db 187 ILSLPPC 193

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-34

Query Match      57.1%; Score 32; DB 6; Length 328;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   1 LMALPPCHAL 10
Db   8 LAGKPKCHAL 17

RESULT 25
US-11-169-041-158
; Sequence 158, Application US/11169041
; Publication No. US2006019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TROSINE
; KINASES AND/OR PROTEIN TROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 158
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-169-041-158

Query Match      57.1%; Score 32; DB 7; Length 400;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   4 LPPCHAL 10
Db   218 LPPPAHI 224

RESULT 26
US-10-880-764-3
; Sequence 3, Application US/10880764
; Publication No. US2006003335A1
; GENERAL INFORMATION:
; APPLICANT: John D. Crispino
; TITLE OF INVENTION: METHODS FOR DIAGNOSTING ACUTE MEGAKARYOBLASTIC LEUKEMIA
; FILE REFERENCE: 27373/3893A
; CURRENT APPLICATION NUMBER: US/10/880,764
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/483,954
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-880-764-3

Query Match      57.1%; Score 32; DB 6; Length 413;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   2 MALPPCHA 9
Db   : |||| |

```

Db 194 LPUPCCEA 201

RESULT 27

US-10-986-501-110

; Sequence 110, Application US/10986501

; Publication No. US20050244845A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

TITLE OF INVENTION: 90 Human Secreted Proteins

FILE REFERENCE: P2013P2CL

CURRENT APPLICATION NUMBER: US/10/986\_501

CURRENT FILING DATE: 2004-11-12

PRIOR FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: 09/1969,730

PRIOR FILING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: 09/1774,639

PRIOR FILING DATE: 2001-02-01

PRIOR APPLICATION NUMBER: 60/238,291

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 09/244,112

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: PCV/US98/16235

PRIOR FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: 60/056,371

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,732

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,366

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,364

PRIOR FILING DATE: 1997-08-19

Remaining Prior Application data removed - See File Wrapper or PALM.

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 373

LENGTH: 457

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: MISC\_FEATURE

NAME/KEY: MISC\_FEATURE

LOCATION: (84)-

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: MISC\_FEATURE

LOCATION: (169)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-986-501-110

Query Match

Score 57.1%; Score 32;

DB 6; Length 457;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPCHA 9

Db 76 PPCHS 80

Query Match

Score 57.1%; Score 32;

DB 6; Length 486;

Best Local Similarity 80.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCH 8

Db 27 APPCH 32

Query Match

Score 57.1%; Score 32;

DB 6; Length 486;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12349431

OTHER INFORMATION: Ceres Seq. ID no.

US-10-667-295-201

Query Match

Score 57.1%; Score 32;

DB 6; Length 486;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCH 8

Db 27 APPCH 32

Query Match

Score 57.1%; Score 32;

DB 6; Length 486;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2580

OTHER INFORMATION: Ceres Seq. ID no.

US-11-072-512-2580

Sequence 2580, Application US/11072512

; Publication No. US2006002945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZURO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KETICHI  
 APPLICANT: IRIE, RIYOTARO  
 APPLICANT: TAMECHIKI, ICHIRO  
 APPLICANT: SEKI, NAONIKO  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: OTSUKA, MOTODU  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: MASUO, YASUHIKO  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT APPLICATION NUMBER: US/11/072,512  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US/60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298  
 PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn ver. 2.1  
 SEQ ID NO: 2580  
 LENGTH: 510  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-072-512-2580

Query Match Score 57.1%; Best Local Similarity 80.0%; Matches 4; Conservative 1; Gaps 0; Indels 0; Length: 510; Software: PatentIn version 3.3  
 Db 204 PPCHA 9  
 Db 204 PPCHA 208

RESULT 31  
 US-10-972-053-2  
 Sequence 2, Application US/10972053  
 Publication No. US20050255489A1  
 GENERAL INFORMATION:  
 APPLICANT: Pierce, James Michael  
 APPLICANT: Kamar, Maria  
 APPLICANT: Lee, Jin-Kyu  
 APPLICANT: Kaneko, Mika  
 TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant  
 CURRENT APPLICATION NUMBER: US/10/972,053  
 CURRENT FILING DATE: 2004-10-22  
 PRIOR APPLICATION NUMBER: PCT/US03/091402  
 PRIOR FILING DATE: 2003-04-23  
 PRIOR APPLICATION NUMBER: US 60/375,172  
 PRIOR FILING DATE: 2002-04-23  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 2  
 LENGTH: 782  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-972-053-2

Query Match Score 57.1%; Best Local Similarity 75.0%; Matches 6; Conservative 0; Gaps 0; Indels 0; Length: 782; Software: PatentIn version 3.3  
 Db 672 AWPPAHAL 679

RESULT 32  
 US-10-972-053-8  
 Sequence 8, Application US/10972053  
 Publication No. US20050255489A1  
 GENERAL INFORMATION:  
 APPLICANT: Pierce, James Michael  
 APPLICANT: Kamar, Maria  
 APPLICANT: Lee, Jin-Kyu  
 APPLICANT: Kaneko, Mika  
 TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant  
 CURRENT APPLICATION NUMBER: US/10/972,053  
 CURRENT FILING DATE: 2004-10-22  
 PRIOR APPLICATION NUMBER: PCT/US03/091402  
 PRIOR FILING DATE: 2003-04-23  
 PRIOR FILING DATE: 2002-04-23  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 8  
 LENGTH: 782  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-972-053-8

Query Match Score 57.1%; Best Local Similarity 75.0%; Matches 6; Conservative 0; Gaps 0; Indels 0; Length: 782; Software: PatentIn version 3.3  
 Db 672 AWPPAHAL 679

RESULT 33  
 US-10-972-053-10  
 Sequence 10, Application US/10972053  
 Publication No. US20050255489A1  
 GENERAL INFORMATION:  
 APPLICANT: Pierce, James Michael  
 APPLICANT: Kamar, Maria  
 APPLICANT: Lee, Jin-Kyu  
 APPLICANT: Kaneko, Mika  
 TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant  
 CURRENT APPLICATION NUMBER: US/10/972,053  
 CURRENT FILING DATE: 2004-10-22  
 PRIOR APPLICATION NUMBER: PCT/US03/091402  
 PRIOR FILING DATE: 2003-04-23  
 PRIOR FILING DATE: 2002-04-23  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 10  
 LENGTH: 784  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-972-053-10

Query Match Score 57.1%; Best Local Similarity 75.0%; Matches 6; Conservative 0; Gaps 0; Indels 0; Length: 784; Software: PatentIn version 3.3  
 Db 674 AWPPAHAL 681

RESULT 34  
Sequence 12, Application US/10972053  
Publication No. US20050255489A1  
GENERAL INFORMATION:  
APPLICANT: Pierce, James Michael  
APPLICANT: Kamar, Maria  
APPLICANT: Lee, Jin-Kyu  
APPLICANT: Kaneko, Mika  
TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant  
FILE REFERENCE: 49-02A  
CURRENT APPLICATION NUMBER: US/10/972,053  
CURRENT FILING DATE: 2004-10-22  
PRIORITY APPLICATION NUMBER: PCT/US03/091102  
PRIOR FILING DATE: 2003-04-23  
PRIORITY APPLICATION NUMBER: US 60/375,172  
PRIOR FILING DATE: 2002-04-23  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 12  
LENGTH: 792  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-972-053-12

Query Match 57.1%; Score 32; DB 7; Length 869;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LMAPPCHAL 10  
Db 707 LBQKPCGGL 716

RESULT 36  
Sequence 2, Application US/11183624  
Publication No. US2005025518A1  
GENERAL INFORMATION:  
APPLICANT: Silos-Santiago, Inmaculada  
TITLE OF INVENTION: Methods and compositions for the treatment and diagnosis of pain disorders using 465566  
FILE REFERENCE: MP101-27221RM  
CURRENT APPLICATION NUMBER: US/11/183,624  
CURRENT FILING DATE: 2005-07-18  
PRIOR APPLICATION NUMBER: US/10/281,866  
PRIOR FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: 60/335,078  
PRIOR FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Fast-SEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 921  
TYPE: PRT  
ORGANISM: Homo sapien

US-11-183-624-2

Query Match 57.1%; Score 32; DB 7; Length 921;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMAPPCC 7  
Db 12 LLAPPCC 18

RESULT 37  
Sequence 70, Application US/11012762  
Publication No. US20050244815A1  
GENERAL INFORMATION:  
APPLICANT: Georgia State University Research Foundation, Inc.  
TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes  
FILE REFERENCE: GSU.PCT  
CURRENT APPLICATION NUMBER: US/11/012,762  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: PCT/US03/19300  
PRIOR FILING DATE: 2003-06-19  
PRIOR APPLICATION NUMBER: US 60/390,046  
PRIOR FILING DATE: 2002-06-19  
NUMBER OF SEQ ID NOS: 133  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 70  
TYPE: PRT  
ORGANISM: Rattus norvegicus

US-11-012-762-70

Query Match 57.1%; Score 32; DB 7; Length 1137;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHAL 10  
Db 675 ALPPAYAL 682

RESULT 35  
Sequence 2532, Application US/11072512  
Publication No. US20060023945A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: OTSUKI, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, KYOTARO  
APPLICANT: TAMECHIKI, ICHIRO  
APPLICANT: SEKI, NAOKICO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOTSUKI  
APPLICANT: NAGAHARA, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIORITY APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2532  
LENGTH: 869  
TYPE: PRT  
ORGANISM: Homo sapiens

RESULT 38  
US-11-198-847-336  
Sequence 336, Application US/11198847  
Publication No. US20050271589A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognex, Inc.  
APPLICANT: Jones, Robert M.  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Olivera, Baldomero M.  
TITLE OF INVENTION: B-Superfamily Conotoxins  
FILE REFERENCE: 2314-236  
CURRENT FILING DATE: 2005-08-08  
PRIOR APPLICATION NUMBER: US 10/198,847  
PRIOR FILING DATE: 2004-05-05  
PRIOR APPLICATION NUMBER: US 10/058,053  
PRIOR FILING DATE: 2000-01-29 226  
PRIOR APPLICATION NUMBER: US 60/264323  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 336  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Conus generalis  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(15)  
OTHER INFORMATION: Xaa may be Phe (D or L)

FEATURE:  
NAME/KEY: DISULFID  
LOCATION: (4)..(14)  
US-11-198-847-336

Query Match  
Best Local Similarity 100.0%; Pred. No. 8.8%; Length 15;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPCH 8  
Db 12 PPCH 15

RESULT 40  
US-11-198-847-334  
Sequence 334, Application US/11198847  
Publication No. US20050271589A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognex, Inc.  
APPLICANT: Jones, Robert M.  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Olivera, Baldomero M.  
TITLE OF INVENTION: B-Superfamily Conotoxins  
FILE REFERENCE: 2314-296  
CURRENT APPLICATION NUMBER: US/11/198,847  
CURRENT FILING DATE: 2005-08-08  
PRIOR APPLICATION NUMBER: US 10/838,226  
PRIOR FILING DATE: 2004-05-05  
PRIOR APPLICATION NUMBER: US 10/058,053  
PRIOR FILING DATE: 2000-01-29  
PRIOR APPLICATION NUMBER: US 60/264323  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 334  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Conus generalis  
FEATURE:  
NAME/KEY: DISULFID  
LOCATION: (4)..(14)  
US-11-198-847-334

Query Match  
Best Local Similarity 100.0%; Pred. No. 9.9%; Length 17;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPCH 8  
Db 12 PPCH 15

RESULT 41  
US-11-198-847-335  
Sequence 335, Application US/11198847  
Publication No. US20050271589A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognex, Inc.  
APPLICANT: Jones, Robert M.  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Olivera, Baldomero M.  
TITLE OF INVENTION: B-Superfamily Conotoxins  
FILE REFERENCE: 2314-236  
CURRENT FILING DATE: 2005-08-08  
PRIOR APPLICATION NUMBER: US 10/838,226  
PRIOR FILING DATE: 2004-05-05  
PRIOR APPLICATION NUMBER: US 60/264323  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 337  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Conus generalis

```

; CURRENT FILING DATE: 2005-08-08
; PRIORITY APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIORITY APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIORITY APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 335
LENGTH: 17
TYPE: PRT
ORGANISM: Conus generalis
FEATURE: DISULFID
NAME/KEY: DISULFID
LOCATION: (6)..(14)
US-11-198-847-335

Query Match 55.4%; Score 31; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPCH 8
Db 12 PPCH 15

RESULT 42
US-11-198-847-235
Sequence 235, Application US/11198847
Publication No. US200502715892A1

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
FILE REFERENCE: 2314-296
CURRENT APPLICATION NUMBER: US/11/198-847
CURRENT FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: US 10/838,226
PRIOR FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 10/058,053
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/264323
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
SEQ ID NO 235
LENGTH: 19
TYPE: PRT
ORGANISM: Conus generalis
US-11-198-847-235

Query Match 55.4%; Score 31; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPCH 8
Db 16 PPCH 19

RESULT 43
US-11-198-847-236
Sequence 236, Application US/11198847
Publication No. US200502715894A1

GENERAL INFORMATION:
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Oliviera, Baldomero M.
TITLE OF INVENTION: B-Superfamily Conotoxins
FILE REFERENCE: 2314-296
CURRENT APPLICATION NUMBER: US/11/198-847
CURRENT FILING DATE: 2005-08-08
PRIOR APPLICATION NUMBER: US 10/838,226
PRIOR FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 10/058,053
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/264323
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.0
SEQ ID NO 236
LENGTH: 19
TYPE: PRT
ORGANISM: Conus vexillum
US-11-198-847-236

Query Match 55.4%; Score 31; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPCH 8
Db 16 PPCH 19

RESULT 44
US-11-120-308-92
Sequence 92, Application US/11120308
Publication No. US2006000527TA1

GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: cDNAs Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120-308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 92
LENGTH: 60
TYPE: PRT
ORGANISM: Triticum aestivum
US-11-120-308-92

Query Match 55.4%; Score 31; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMALPP 6

```

Db 43 LMALPP 48      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45  
US-11-198-847-14  
; Sequence 14, Application US/11198847  
; Publication No. US20050271589A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognex, Inc.  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; TITLE OF INVENTION: B-Superfamily Conotoxins  
; FILE REFERENCE: 2314-296  
; CURRENT APPLICATION NUMBER: US/11/198,847  
; CURRENT FILING DATE: 2005-08-08  
; PRIOR APPLICATION NUMBER: US 10/838,226  
; PRIOR FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: US 10/058,053  
; PRIOR FILING DATE: 2000-01-29  
; PRIOR APPLICATION NUMBER: US 60/264323  
; NUMBER OF SEQ ID NOS: 340  
; SEQ ID NO: 14  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Conus generalis  
; US-11-198-847-14

Query Match 55.4%; Score 31; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPCH 8  
Db 67 PPCH 70

RESULT 46  
US-11-198-847-221  
; Sequence 221, Application US/11198847  
; Publication No. US20050271589A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognex, Inc.  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; TITLE OF INVENTION: B-Superfamily Conotoxins  
; FILE REFERENCE: 2314-296  
; CURRENT APPLICATION NUMBER: US/11/198,847  
; CURRENT FILING DATE: 2005-08-08  
; PRIOR APPLICATION NUMBER: US 10/838,226  
; PRIOR FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: US 10/058,053  
; PRIOR FILING DATE: 2000-01-29  
; PRIOR APPLICATION NUMBER: US 60/264323  
; NUMBER OF SEQ ID NOS: 340  
; SEQ ID NO: 221  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Conus vexillum  
; US-11-198-847-221

Query Match 55.4%; Score 31; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 38;

Qy 5 PPCH 8  
Db 67 PPCH 70

RESULT 47  
US-10-498-026-27  
; Sequence 27, Application US/10498026  
; Publication No. US20060024334A1  
; GENERAL INFORMATION:  
; APPLICANT: CIRCASTA LIMITED  
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS  
; FILE REFERENCE: N.8730 WO GCM  
; CURRENT APPLICATION NUMBER: US/10/498,026  
; CURRENT FILING DATE: 2004-06-04  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 27  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Felis domesticus  
; US-10-498-026-27

Query Match 55.4%; Score 31; DB 6; Length 88;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALPPC 7  
Db 5 ALPPC 9

RESULT 48  
US-11-033-039-135  
; Sequence 135, Application US/11033039  
; Publication No. US20060002347A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/395,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO: 135  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Felis catus  
; US-11-033-039-135

Query Match 55.4%; Score 31; DB 7; Length 88;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ALPPC 7  
Db 5 ALPPC 9

RESULT 49  
US-11-072-512-765  
; Sequence 3765, Application US/11072512  
; Publication No. US2006029945A1  
; GENERAL INFORMATION:

Query Match 55.4%; Score 31; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 38;

APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKI, ICHIRO  
 APPLICANT: SEKI, NAOHIKO  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: MOTOYUKI  
 APPLICANT: MASUHO, YASUHIKO  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT APPLICATION NUMBER: US/11/072,512  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US 60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298  
 PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 3765  
 LENGTH: 104  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-072-512-3765

PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2406  
 LENGTH: 125  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-072-512-2406

Query Match 55.4%; Score 31; DB 7; Length 125;  
 Best Local Similarity 71.4%; Pred. No. 63;  
 Matches 5; Conservative 1; Mismatches 1;  
 Indels 0; Gaps 0;

Qy |||||  
 Db 42 LPPAHSI 48

Search completed: February 17, 2006, 02:48:29  
 Job time : 21 secs

RESULT 50  
 US-11-072-512-2406  
 Sequence 2406 Application US/11072512  
 Publication No. US2006029945A1  
 GENERAL INFORMATION:  
 APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKI, ICHIRO  
 APPLICANT: SEKI, NAOHIKO  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: MOTOYUKI  
 APPLICANT: MASUHO, YASUHIKO  
 APPLICANT: NAGAHARI, KENJI  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT APPLICATION NUMBER: US/11/072,512  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US 60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298  
 PRIOR FILING DATE: 2001-11-05

Query Match 55.4%; Score 31; DB 7; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 4; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy |||||  
 Db 90 PPCH 93

RESULT 50  
 US-11-072-512-2406  
 Sequence 2406 Application US/11072512  
 Publication No. US2006029945A1  
 GENERAL INFORMATION:  
 APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKI, ICHIRO  
 APPLICANT: SEKI, NAOHIKO  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: MOTOYUKI  
 APPLICANT: MASUHO, YASUHIKO  
 APPLICANT: NAGAHARI, KENJI  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT APPLICATION NUMBER: US/11/072,512  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US 60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298

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## OM protein - protein search, using sw model

Run on: Run on: February 17, 2006, 02:44:41 ; Search time 165 Seconds

(without alignments)

25.323 Million cell updates/sec

Title: US-10-734-049B-188  
 Perfect score: 56

Sequence: 1 LMAUPCHAL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

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2: /cgn2\_6/\_ptodata/1/pubpaas/US08\_PUBCOMB.pep:\*\*

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5: /cgn2\_6/\_ptodata/1/pubpaas/US10B\_PUBCOMB.pep:\*\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	56	100.0	18	4	US-10-623-313-150	Sequence 150, App	Sequence 150, App	376
4	56	100.0	216	5	US-10-450-763-51128	Sequence 51128, A	Sequence 51128, A	377
5	56	100.0	313	4	US-10-308-192-5	Sequence 5, Appli	Sequence 5, Appli	378
6	56	100.0	313	4	US-10-313-142	Sequence 142, App	Sequence 142, App	379
7	56	100.0	313	5	US-10-733-878-433	Sequence 433, App	Sequence 433, App	380
8	56	100.0	313	5	US-10-733-860-1171	Sequence 1171, App	Sequence 1171, App	381
9	56	100.0	313	5	US-10-734-049B-267	Sequence 267, App	Sequence 267, App	382
10	56	100.0	313	5	US-10-756-149-4996	Sequence 4996, App	Sequence 4996, App	383
11	52	92.9	264	4	US-10-284-122A-66040	Sequence 66040, A	Sequence 66040, A	384
12	52	92.9	264	4	US-10-283-122A-66163	Sequence 66163, A	Sequence 66163, A	385
13	52	92.9	266	4	US-10-282-122A-65128	Sequence 65128, A	Sequence 65128, A	386
14	49	87.5	314	4	US-10-284-122A-61012	Sequence 61012, A	Sequence 61012, A	387
15	48	85.7	109	4	US-10-424-599-247816	Sequence 247816,	Sequence 247816,	388
16	48	85.7	154	4	US-10-424-599-247814	Sequence 247814,	Sequence 247814,	389
17	48	85.7	263	4	US-10-284-122A-64769	Sequence 64769, A	Sequence 64769, A	390
18	48	85.7	266	4	US-10-283-122A-61002	Sequence 61002, A	Sequence 61002, A	391
19	48	85.7	266	4	US-10-282-122A-62895	Sequence 62895, A	Sequence 62895, A	392
20	48	85.7	266	4	US-10-284-122A-63879	Sequence 63877, A	Sequence 63877, A	393
21	48	85.7	314	4	US-10-283-122A-64533	Sequence 45383, A	Sequence 45383, A	394
22	48	85.7	315	5	US-10-501-282-1160	Sequence 1160, App	Sequence 1160, App	395
23	48	85.7	321	6	US-11-09-143-5883	Sequence 5883, App	Sequence 5883, App	396
24	48	85.7	333	5	US-10-779-597-23	Sequence 23, Appli	Sequence 23, Appli	397
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26	48	85.7	530	4	US-10-424-599-247813	Sequence 247813,	Sequence 247813,	399
27	48	85.7	530	4	US-10-424-599-247817	Sequence 247817,	Sequence 247817,	400

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48	82.6	136	3	US-09-467-550-396
49	82.6	136	3	US-09-467-550-396
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109	137	66.1	279	Sequence 8419, Ap	182	35	US-10-425-115-24449	Sequence 216449,	
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115	484	4	US-10-425-115-295538	Sequence 295538,	188	35	US-10-437-963-179096	Sequence 179096,	
116	823	4	US-10-437-963-167023	Sequence 167023,	189	35	US-10-437-963-139916	Sequence 139916,	
117	1138	4	US-10-437-963-178269	Sequence 178269,	190	35	US-10-425-115-396194	Sequence 264194,	
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119	136	4	US-10-408-167-1987	Sequence 1987, Ap	192	35	US-10-437-963-126976	Sequence 126976,	
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123	79	4	US-10-425-115-235232	Sequence 23522,	196	35	US-10-425-115-368073	Sequence 368073,	
124	89	4	US-10-425-115-331150	Sequence 331150,	197	35	US-10-425-115-71277	Sequence 41727,	
125	90	4	US-10-424-599-165755	Sequence 165755,	198	35	US-10-437-963-17714	Sequence 107714,	
126	92	4	US-10-437-963-107346	Sequence 107346,	199	35	US-10-425-115-2507	Sequence 2507, Ap	
127	102	4	US-10-425-115-318482	Sequence 318482,	200	35	US-10-1-94-446	Sequence 446, App	
128	102	5	US-10-926-093-20	Sequence 20, Appl	201	35	US-10-425-115-37580	Sequence 337580,	
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131	111	4	US-10-028-091-5	Sequence 5, Appli	204	35	US-10-296-115-1476	Sequence 1476, Ap	
132	111	4	US-10-090-049-5	Sequence 5, Appli	205	35	US-10-437-963-185043	Sequence 185043,	
133	111	4	US-10-014-055-5	Sequence 5, Appli	206	35	US-10-425-115-21690	Sequence 241690,	
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140	151	4	US-10-425-115-338924	Sequence 338924,	213	35	US-10-188-832-91	Sequence 191822,	
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146	276	4	US-10-425-115-230233	Sequence 230233,	219	35	US-10-437-963-155050	Sequence 165050,	
147	289	4	US-10-425-114-521212	Sequence 52412, A	220	35	US-10-425-114-393905	Sequence 393905,	
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149	318	5	US-10-678-639-31	Sequence 31, Appli	222	35	US-10-28-122A-50418	Sequence 50418, A	
150	319	3	US-09-847-102A-61	Sequence 61, Appli	223	35	US-10-425-133410	Sequence 323410,	
151	349	4	US-10-425-115-23941	Sequence 23941, A	224	35	US-10-425-115-34216	Sequence 48216, A	
152	351	4	US-10-425-114-69011	Sequence 69011, A	225	35	US-10-437-963-156216	Sequence 21, Appli	
153	64.3	64.3	US-10-437-963-107575	Sequence 10575,	226	35	US-10-425-114-334216	Sequence 165050,	
154	544	3	US-09-847-102A-40	Sequence 40, Appli	227	35	US-10-425-115-34216	Sequence 21, Appli	
155	626	3	US-09-847-102A-45	Sequence 45, Appli	228	35	US-10-425-115-343410	Sequence 21, Appli	
156	635	4	US-10-428-122A-75520	Sequence 78520, A	229	35	US-10-428-122A-88216	Sequence 21, Appli	
157	64.3	64.3	US-09-847-102A-44	Sequence 44, Appli	230	35	US-10-437-963-14161	Sequence 165050,	
158	64.3	64.3	US-10-385-976-39	Sequence 39, Appli	231	35	US-10-437-963-156216	Sequence 21, Appli	
159	64.3	64.3	US-10-287-46A-466	Sequence 466, Appli	232	35	US-10-425-114-334216	Sequence 21, Appli	
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**ALIGNMENTS**  
  
**RESULT 1**  
 US-10-734-049A-188      Sequence 188, Application US/10734049A  
 ; Publication No. US20050042624A1  
 ; GENERAL INFORMATION:  
 ;      APPLICANT: ITOH, Kyogo  
 ;      TITLE OF INVENTION: TUMOR ANTIGEN  
 ;      FILE REFERENCE: Q\_78182  
 ;      CURRENT APPLICATION NUMBER: US/10/734,049A  
 ;      CURRENT FILING DATE: 2003-12-12  
 ;      PRIOR APPLICATION NUMBER: PCT/JP02/05799  
 ;      PRIOR FILING DATE: 2002-06-11  
 ;      PRIOR APPLICATION NUMBER: JP 2001/17705B  
 ;      PRIOR FILING DATE: 2001-06-12  
 ;      PRIOR APPLICATION NUMBER: JP 2001/25072B  
 ;      PRIOR FILING DATE: 2001-08-21  
 ;      NUMBER OF SEQ ID NOS: 408  
 ;      SOFTWARE: PatentIn version 3.3  
 ;      SEQ ID NO: 188  
 ;      LENGTH: 10  
 ;      TYPE: PRT  
 ;      ORGANISM: Artificial  
 ;      OTHER INFORMATION: Designed peptide recognized by HLA-A2 restricted cytotoxic T  
 ;      OTHER INFORMATION: Lymphocytes  
 ;      OTHER INFORMATION: PatentIn version 3.3  
  
**RESULT 2**  
 US-10-734-049A-188      Sequence 146, Application US/10629313  
 ; Publication No. US2004176572A1  
 ; GENERAL INFORMATION:  
 ;      APPLICANT: Nelson B. Freimer  
 ;      TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18  
 ;      FILE REFERENCE: UCAL-154CIP5  
 ;      CURRENT APPLICATION NUMBER: US/10/629,313  
 ;      CURRENT FILING DATE: 2003-07-28  
 ;      PRIOR APPLICATION NUMBER: 09/722,544  
 ;      PRIOR FILING DATE: 2000-11-28  
 ;      PRIOR APPLICATION NUMBER: 09/631,275  
 ;      PRIOR FILING DATE: 2000-06-02  
 ;      PRIOR APPLICATION NUMBER: 09/268,992  
 ;      PRIOR FILING DATE: 1999-03-16  
 ;      PRIOR APPLICATION NUMBER: 09/236,134  
 ;      PRIOR FILING DATE: 1999-01-22  
 ;      PRIOR APPLICATION NUMBER: 60/078,044  
 ;      PRIOR FILING DATE: 1998-03-16  
 ;      PRIOR APPLICATION NUMBER: 60/088,312  
 ;      PRIOR FILING DATE: 1998-06-05  
 ;      PRIOR APPLICATION NUMBER: 60/106,056  
 ;      PRIOR FILING DATE: 1998-10-28  
 ;      NUMBER OF SEQ ID NOS: 165  
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 ;      SEQ ID NO: 146  
 ;      LENGTH: 18  
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**RESULT 3**  
 US-10-629-313-150      Query Match 100.0%; Score 56; DB 4; Length 18;  
 ;      Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;  
 ;      Matches 10; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
 ;      Qy      1 LMALPPCHAL 10  
 ;      Db      3 LMALPPCHAL 12  
  
**RESULT 4**  
 US-10-629-313-150      Sequence 150, Application US/10629313  
 ;      Publication No. US20040176572A1  
 ;      GENERAL INFORMATION:  
 ;      APPLICANT: Nelson B. Freimer  
 ;      TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18  
 ;      FILE REFERENCE: UCAL-154CIP5  
 ;      CURRENT APPLICATION NUMBER: US/10/629,313  
 ;      CURRENT FILING DATE: 2003-07-28  
 ;      PRIOR APPLICATION NUMBER: 09/722,544  
 ;      PRIOR FILING DATE: 2000-06-02  
 ;      PRIOR APPLICATION NUMBER: 09/268,992  
 ;      PRIOR FILING DATE: 1999-03-16  
 ;      PRIOR APPLICATION NUMBER: 09/236,134  
 ;      PRIOR FILING DATE: 1999-01-22  
 ;      PRIOR APPLICATION NUMBER: 60/078,044  
 ;      PRIOR FILING DATE: 1998-03-16  
 ;      PRIOR APPLICATION NUMBER: 60/088,312  
 ;      PRIOR FILING DATE: 1998-06-05  
 ;      PRIOR APPLICATION NUMBER: 60/106,056  
 ;      PRIOR FILING DATE: 1998-10-28  
 ;      NUMBER OF SEQ ID NOS: 165  
 ;      SOFTWARE: PastSEQ for Windows Version 4.0  
 ;      SEQ ID NO: 146  
 ;      LENGTH: 18  
 ;      TYPE: PRT  
 ;      ORGANISM: Homo sapiens  
 ;      US-10-629-313-146  
  
**RESULT 5**  
 US-10-629-313-150      Query Match 100.0%; Score 56; DB 4; Length 18;  
 ;      Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;  
 ;      Matches 10; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
 ;      Qy      1 LMALPPCHAL 10  
 ;      Db      3 LMALPPCHAL 12

SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 150  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-629-313-150

Query Match	100.0%	Score 56;	DB 4;	Length 18;
Best Local Similarity	100.0%	Pred. No. 0.052;	Indels 0;	Gaps 0;
Matches 10;	Conservative 0;	Mismatches 0;		
Qy	1 LMALPPCHAL 10			
Db	3 LMALPPCHAL 12			

RESULT 4  
US-10-450-763-51128  
; Sequence 51128, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790C1P3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 51128  
; LENGTH: 216  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: DOMAIN  
; NAME/KEY: DOMAIN  
; LOCATION: (1.33)..(1.82)  
; OTHER INFORMATION: Thymidylate synthase proteins domain identified by eMATRIX,  
; accession number BL000091E, p-value=9.813e-32, raw score of 22.23  
; OTHER INFORMATION: accession number BL000091E, p-value=9.813e-32, raw score of 22.23  
; FEATURE: DOMAIN  
; NAME/KEY: DOMAIN  
; LOCATION: (112)..(216)  
; OTHER INFORMATION: Thymidylate synthase domain identified by PFam, accession  
; number BL000091E, p-value=1.3e-68, PFam score of 241.44  
US-10-450-763-51128

Query Match

Best Local Similarity	100.0%	Score 56;	DB 5;	Length 216;
Matches 10;	Conservative 0;	Pred. No. 0.49;	Indels 0;	Gaps 0;
Qy	1 LMALPPCHAL 10			
Db	116 LMALPPCHAL 125			

RESULT 5  
US-10-308-192-5  
; Sequence 5, Application US/10308192  
; Publication No. US20030224985A1  
; GENERAL INFORMATION:  
; APPLICANT: Loeb, Lawrence  
; APPLICANT: Werner, Geurtzen  
; TITLE OF INVENTION: Novel Thymidylate Synthase Mutants  
; FILE REFERENCE: 03100132aa  
; CURRENT APPLICATION NUMBER: US/10/308,192  
; CURRENT FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5

; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-308-192-5

Query Match	100.0%	Score 56;	DB 4;	Length 313;
Best Local Similarity	100.0%	Pred. No. 0.69;	Indels 0;	Gaps 0;
Matches 10;	Conservative 0;	Mismatches 0;		
Qy	1 LMALPPCHAL 10			
Db	189 LMALPPCHAL 198			

RESULT 6  
US-10-629-313-142  
; Sequence 142, Application US/10629313  
; Publication No. US20040176572A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelson B. Freimer  
; APPLICANT: Hong Chen  
; APPLICANT: Victor I. Reus  
; APPLICANT: Susan K. Service  
; APPLICANT: Lynne Alison McInnes  
; APPLICANT: Pedro Leon  
; APPLICANT: Lodewijk Sandkuyl  
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-1  
; TITLE OF INVENTION: Related Disorders  
; FILE REFERENCE: UGAL1541TPS  
; CURRENT APPLICATION NUMBER: US/10/629,313  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: 09/722,544  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/631,275  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 09/268,992  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/078,044  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 60/088,312  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/106,056  
; PRIOR FILING DATE: 1998-10-28  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 142  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-629-313-142

Query Match	100.0%	Score 56;	DB 4;	Length 313;
Best Local Similarity	100.0%	Pred. No. 0.69;	Indels 0;	Gaps 0;
Matches 10;	Conservative 0;	Mismatches 0;		
Qy	1 LMALPPCHAL 10			
Db	189 LMALPPCHAL 198			

RESULT 7  
US-10-73-878-433  
; Sequence 433, Application US/10733878  
; Publication No. US200402440A1  
; GENERAL INFORMATION:  
; APPLICANT: Jean-Philippe Girard  
; APPLICANT: Francois Ahnric  
; APPLICANT: Myriam Roussigne  
; APPLICANT: Thomas Clouaire  
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR  
; CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL  
; TITLE OF INVENTION:

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; TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BLOBANK_012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 433
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-878-433

Query Match          100.0%;  Score 56;  DB 5;  Length 313;
Best Local Similarity 100.0%;  Pred. No. 0.69;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 8
US-10-723-86-0-1171
Sequence 1171, Application US/107238860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
APPLICANT: Ginsburg, Wendy M.
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR FILING NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SEQ ID NO: 1171
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-1171

Query Match          100.0%;  Score 56;  DB 5;  Length 313;
Best Local Similarity 100.0%;  Pred. No. 0.69;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 9
US-10-734-049A-267
Sequence 267, Application US/10734049A
Publication No. US20050042624A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
APPLICANT: SHICHIJO, Shigeki
TITLE OF INVENTION: TUMOR ANTIGEN
CURRENT FILING NUMBER: US/10/734,049A
CURRENT FILING DATE: 2003-12-12
PRIOR APPLICATION NUMBER: PCT/JP2002/05799
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: JP 2001/177058
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2001/250728

; PRIORITY: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 267
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-049A-267

Query Match          100.0%;  Score 56;  DB 5;  Length 313;
Best Local Similarity 100.0%;  Pred. No. 0.69;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 1MALPPCHAL 10
Db      189 1MALPPCHAL 198

RESULT 10
US-10-756-149-4996
Sequence 4996, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
TITLE OF INVENTION: NOVEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 4996
LENGTH: 313
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149-4996

Query Match          100.0%;  Score 56;  DB 5;  Length 313;
Best Local Similarity 100.0%;  Pred. No. 0.69;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 1MALPPCHAL 10
Db      189 1MALPPCHAL 198

RESULT 11
US-10-282-122A-66040
Sequence 66040, Application US/10282122A
Publication No. US2004029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forgyrh, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA_034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-13
PRIOR APPLICATION NUMBER: 60/207,727

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; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: 60/230,335
; PRIORITY FILING DATE: 2000-09-06
; PRIORITY APPLICATION NUMBER: 60/230,347
; PRIORITY FILING DATE: 2000-09-09
; PRIORITY APPLICATION NUMBER: 60/242,578
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 60/253,625
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: 60/267,636
; PRIORITY FILING DATE: 2001-02-09
; PRIORITY APPLICATION NUMBER: 60/269,308
; PRIORITY FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66040
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-282-122A-66040

Query Match 92.9%; Score 52; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 141 MALPPCHAL 149

RESULT 12
US-10-282-122A-66163
; Sequence 66163, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cherry
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-16
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66163
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-66163

Query Match 92.9%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 MALPPCHAL 10
Db 143 MALPPCHAL 151

RESULT 14
US-10-282-122A-61012
; Sequence 61012, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EIJTRA_034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 61/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-7
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO: 61012
LENGTH: 314
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-10-282-122A-61012

Query Match 87.5%; Score 49; DB 4; Length 314;
Best Local Similarity 98.9%; Pred. No. 8.8;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
SEQ ID NO: 247816
LENGTH: 109
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(109)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65808C.1.pep
US-10-424-599-247816

Query Match 85.7%; Score 48; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
SEQ ID NO: 247816
LENGTH: 109
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(109)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65808C.1.pep
US-10-424-599-247816

Query Match 85.7%; Score 48; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
SEQ ID NO: 247814
LENGTH: 154
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(154)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

Query Match 85.7%; Score 48; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
SEQ ID NO: 247814
LENGTH: 154
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(154)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

RESULT 15
US-10-424-599-247814
; Sequence 247814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-2-(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285584
; SEQ ID NO: 247814
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .(154)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

Query Match 85.7%; Score 48; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
SEQ ID NO: 247814
LENGTH: 154
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(154)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

RESULT 16
US-10-424-599-247814
; Sequence 247814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-2-(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285584
; SEQ ID NO: 247814
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .(154)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

Query Match 85.7%; Score 48; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
SEQ ID NO: 247814
LENGTH: 154
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) .(154)
OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

RESULT 17
US-10-282-122A-64769
; Sequence 64769, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsien, Kari

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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITA:034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO: 64769
LENGTH: 263
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64769

RESULT 18
US-10-282-122A-61802 ; sequence 61802, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITA:034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848

```

PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22--  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SBO ID NO: 61802  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Mycobacterium avium  
S-10-282-122A-61802

Query Match 85.7% Score  
Best Local Similarity 100.0% Pred  
Matches 8; Conservative 0; Mi

y	2	MA1PPCHA	9
b	144	MA1PPCHA	151

RESULT 19  
S-10-282-122A-62695  
Sequence 62695, Application US/1028211  
Publication No. US2004029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangshu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karin  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of FILE REFERENCE: ELITA-034A  
CURRENT APPLICATION NUMBER: US/10/28211  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22--  
PRIOR APPLICATION NUMBER: 60/267,636

```

; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 62695
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62695

Query Match 85.7%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 21
US-10-282-122A-45383
; Sequence 43383, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Travick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA-044A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,315
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 63877
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63877

Query Match 85.7%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1;
Indels 0; Gaps 0;

Query Match 85.7%; Score 48; DB 4; Length 314;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1;
Indels 0; Gaps 0;

```

Qy 2 MALPPCHL 10  
Db 191 MALPPCTL 199

RESULT 22  
US-10-501-282-1160  
; Sequence 1160, Application US/10501282  
; Publication No. US2005020328041  
GENERAL INFORMATION  
APPLICANT: MCMICHAEL, JOHN CALHOUN  
APPLICANT: ZAGURSKY, ROBERT JOHN  
APPLICANT: RUSSELL, DAVID PARRISH  
APPLICANT: FLETCHER, LEAH DIANE  
TITLE OF INVENTION: ALLOIОСОССУS OTITIDIS OPEN READING FRAMES (ORFs) ENCODING FILE REFERENCE: AM100780 L2  
CURRENT APPLICATION NUMBER: US/10/501-282  
CURRENT FILING DATE: 2004-07-09  
PRIOR APPLICATION NUMBER: 60/1333,777  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: 60/1426,742  
PRIOR FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: PCT/US02/36123  
PRIOR FILING DATE: 2002-11-25  
NUMBER OF SEQ ID NOS: 6653  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1160  
LENGTH: 315  
TYPE: PRT  
ORGANISM: Alloioсоссус otitidis  
US-10-501-282-1160

Query Match 85.7%; Score 48; DB 5; Length 315;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHL 10  
Db 192 MALPPCTL 200

RESULT 23  
US-11-097-143-5883  
; Sequence 5883, Application US/11097143  
; Publication No. US20050208558A1  
GENERAL INFORMATION  
APPLICANT: Venter, J. Craig  
APPLICANT: et al.  
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE TITLE OF INVENTION: DROSOPHILA GENES.  
FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: 60/157,832  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/160,191  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/161,932  
PRIOR FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: 60/164,769  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/173,383  
PRIOR FILING DATE: 1999-12-08  
PRIOR APPLICATION NUMBER: 60/175,693  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: 60/184,831  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/191,637  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FASTSEQ for Windows Version 4.0

Query Match 85.7%; Score 48; DB 5; Length 333;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHL 10  
Db 210 MALPPCHVL 218

RESULT 24  
US-10-779-597-23  
; Sequence 23, Application US/10779597  
; Publication No. US2004023495A1  
GENERAL INFORMATION  
APPLICANT: Oregon Health & Science University  
APPLICANT: Wong, Scott W.  
APPLICANT: Axthelm, Michael K.  
APPLICANT: Hansen, Scott G.  
TITLE OF INVENTION: JAPANESE MACAQUE HERPESVIRUS NUCLEIC ACID SEQUENCES AND THEIR USE  
FILE REFERENCE: 178-67426  
CURRENT APPLICATION NUMBER: US/10/779,597  
CURRENT FILING DATE: 2004-02-12  
PRIOR APPLICATION NUMBER: 10/276,524  
PRIOR FILING DATE: 2003-11-13  
PRIOR APPLICATION NUMBER: PCT/US01/16274  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: 60/205,652  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 23  
LENGTH: 333  
TYPE: PRT  
ORGANISM: Japanese Macaque Herpesvirus  
US-10-779-597-23

Query Match 85.7%; Score 48; DB 5; Length 333;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHL 10  
Db 210 MALPPCHVL 218

RESULT 25  
US-10-320-797-3118  
; Sequence 3118, Application US/10320797  
; Publication No. US2004014955A1  
GENERAL INFORMATION  
APPLICANT: Zamudio, Carlos  
APPLICANT: Eroshkin, Alexey M.  
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND METHODS OF USE  
FILE REFERENCE: 10182-021-999  
CURRENT APPLICATION NUMBER: US/10/320,797  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: 60/182-021-999  
PRIOR FILING DATE: 2001-12-17  
NUMBER OF SEQ ID NOS: 3361  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3118  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Cryptococcus neoformans  
FEATURE: MIS\_C\_FEATURE  
NAME/KEY: MIS\_C\_FEATURE

; LOCATION: (271)..(271)  
; OTHER INFORMATION: xaa = any amino acid  
 US-10-320-797-3118

Query Match      85.7%;    Score 48;    DB 4;    Length 350;  
 Best Local Similarity 100.0%;    Pred. No. 14;  
 Matches 8;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 Qy      1 LMALPPCH 8  
 Db      192 LMALPPCH 199

RESULT 26  
 US-10-424-599-247813  
; Sequence 247813, Application US/10424599  
; Publication No. US2004031072A1  
; GENERAL INFORMATION:  
;   APPLICANT: La Rosa, Thomas J  
;   APPLICANT: Kovalic, David K  
;   APPLICANT: Zhou, Yihua  
;   APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; SEQ ID NO 247813  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_65805C.1.pep  
 US-10-424-599-247813

Query Match      85.7%;    Score 48;    DB 4;    Length 530;  
 Best Local Similarity 100.0%;    Pred. No. 20;  
 Matches 8;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 Qy      1 LMALPPCH 8  
 Db      406 LMALPPCH 413

RESULT 27  
 US-10-424-599-247817  
; Sequence 247817, Application US/10424599  
; Publication No. US2004031072A1  
; GENERAL INFORMATION:  
;   APPLICANT: La Rosa, Thomas J  
;   APPLICANT: Kovalic, David K  
;   APPLICANT: Zhou, Yihua  
;   APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; SEQ ID NO 247817  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_65809C.1.pep  
 US-10-424-599-247817

RESULT 28  
 US-10-425-114-49649  
; Sequence 49649, Application US/10425114  
; Publication No. US2004034888A1  
; GENERAL INFORMATION:  
;   APPLICANT: Liu, Jingdong  
;   APPLICANT: Zhou, Yihua  
;   APPLICANT: Kovacic, David K.  
;   APPLICANT: Screen, Steven E.  
;   APPLICANT: Tabaska, Jack E.  
;   APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 49649  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3051-050-G2\_FLI.pep  
 US-10-425-114-49649

Query Match      85.7%;    Score 48;    DB 4;    Length 579;  
 Best Local Similarity 100.0%;    Pred. No. 22;  
 Matches 8;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 Qy      1 LMALPPCH 8  
 Db      455 LMALPPCH 462

RESULT 29  
 US-09-954-197-2  
; Sequence 2, Application US/09954197  
; Patent No. US2002107379A1  
; GENERAL INFORMATION:  
;   APPLICANT: MARK, Achim  
;   APPLICANT: MARX, Achim  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE thyA GENE  
; FILE REFERENCE: 032301 WD 201  
; CURRENT APPLICATION NUMBER: US/09/954,197  
; CURRENT FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
 US-09-954-197-2

Query Match      83.9%;    Score 47;    DB 3;    Length 266;  
 Best Local Similarity 88.9%;    Pred. No. 16;  
 Matches 8;    Conservative 0;    Mismatches 1;    Indels 0;    Gaps 0;  
 Qy      2 MALPCHAL 10  
 Db      144 MALPCHL 152

RESULT 30  
 US-09-738-626-4442  
; Sequence 4442, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
;   APPLICANT: NAKAGAWA, SATOSHI  
;   APPLICANT: MIZOGUCHI, HIROSHI  
;   APPLICANT: ANDO, SEIKO

Query Match      85.7%;    Score 48;    DB 4;    Length 530;  
 Best Local Similarity 100.0%;    Pred. No. 20;  
 Matches 8;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 Qy      1 LMALPPCH 8

APPLICANT: HAYASHI, MIKIRO  
 APPLICANT: OCHIAI, KEIKO  
 APPLICANT: YOKOI, HARUHIKO  
 APPLICANT: TATEISHI, NAOKO  
 APPLICANT: SENOH, AKIHIRO  
 APPLICANT: IKEDA, MASATO  
 APPLICANT: OZAKI, AKIO  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-125  
 CURRENT APPLICATION NUMBER: US/09/738,626  
 CURRENT FILING DATE: 2000-12-18  
 PRIOR APPLICATION NUMBER: JP 99/377484  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: JP 00/159162  
 PRIOR FILING DATE: 2000-04-07  
 NUMBER OF SEQ ID NOS: 70-59  
 SOFTWARE: PatentIn ver. 3.0  
 SEQ ID NO: 4442  
 LENGTH: 266  
 TYPE: PRT  
 ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-4442

Query Match 83.9%; Score 47; DB 3; Length 266;  
 Best Local Similarity 88.9%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 144 MALPPCHAL 152

RESULT 31  
 US-10-282-122A-53671  
 Sequence 53671, Application US/10282122A  
 Publication No. US20040029129A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cherry  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA-034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-06  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 50921  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Bordetella pertussis  
 US-10-282-122A-50921

Query Match 83.9%; Score 47; DB 4; Length 323;  
 Best Local Similarity 88.9%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**RESULT 33**  
 US-10-282-122A-67673 Application US/10282122A  
 Publication No. US2004029129A1

**GENERAL INFORMATION:**

- APPLICANT: Wang, Liangsu
- APPLICANT: Zamudio, Carlos
- APPLICANT: Malone, Cheryl
- APPLICANT: Haselbeck, Robert
- APPLICANT: Ohlsen, Kari
- APPLICANT: Zyskind, Judith
- APPLICANT: Wall, Daniel
- APPLICANT: Trawick, John
- APPLICANT: Carr, Grant
- APPLICANT: Yamamoto, Robert
- APPLICANT: Forsyth, R.
- APPLICANT: Xu, H.

**TITLE OF INVENTION: Identification of Essential Genes in Microorganisms**

**FILE REFERENCE: ELITRA 034A**

**CURRENT FILING DATE: 2003-02-20**

**PRIOR APPLICATION NUMBER: 60/191,078**

**PRIOR FILING DATE: 2000-03-21**

**PRIOR APPLICATION NUMBER: 60/206,848**

**PRIOR FILING DATE: 2000-05-23**

**PRIOR APPLICATION NUMBER: 60/207,727**

**PRIOR FILING DATE: 2000-05-26**

**PRIOR APPLICATION NUMBER: 60/230,335**

**PRIOR FILING DATE: 2000-09-06**

**PRIOR APPLICATION NUMBER: 60/230,347**

**PRIOR FILING DATE: 2000-09-09**

**PRIOR APPLICATION NUMBER: 60/242,578**

**PRIOR FILING DATE: 2000-10-23**

**PRIOR APPLICATION NUMBER: 60/253,625**

**PRIOR FILING DATE: 2000-11-27**

**PRIOR APPLICATION NUMBER: 60/257,931**

**PRIOR FILING DATE: 2000-12-22**

**PRIOR APPLICATION NUMBER: 60/267,636**

**PRIOR FILING DATE: 2001-02-09**

**PRIOR APPLICATION NUMBER: 60/269,308**

**PRIOR FILING DATE: 2001-02-16**

**Remaining Prior Application data removed - See File Wrapper or PALM.**

**NUMBER OF SEQ ID NOS: 78614**

**SOFTWARE: PatentIn version 3.1**

**SEQ ID NO: 69408**

**LENGTH: 323**

**TYPE: PRT**

**ORGANISM: Pseudomonas syringae**

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**RESULT 35**  
 US-10-282-122A-69408

**GENERAL INFORMATION:**

- APPLICANT: Edwards, Alfred
- APPLICANT: Dharamsi, Akil
- APPLICANT: Vedadi, Masoud
- APPLICANT: Alam, Muhammad Zahoor
- APPLICANT: Armstrong, Cheryl
- APPLICANT: Awrey, Donald B.
- APPLICANT: Beattie, Bryan
- APPLICANT: Buzadija, Kristina
- APPLICANT: Canadien, Veronica
- APPLICANT: Domagala, Megan
- APPLICANT: Houston, Simon
- APPLICANT: Kanagarajah, Dushy
- APPLICANT: Li, Qin
- APPLICANT: Mansouri, Kamran
- APPLICANT: McDonald, Merry-Lynn
- APPLICANT: Netter, Kathleen
- APPLICANT: Ng, Ivy

**Query Match 83.9%; Score 47; DB 4; Length 323;**

**Best Local Similarity 88.9%; Pred. No. 19; Mismatches 0; Gaps 0;**

**Matches 8; Conservative 0; Indels 1;**

**Remaining Prior Application data removed - See File Wrapper or PALM.**

**NUMBER OF SEQ ID NOS: 78614**

**SOFTWARE: PatentIn version 3.1**

**SEQ ID NO: 67673**

**LENGTH: 323**

**TYPE: PRT**

**ORGANISM: Pseudomonas putida**

---

**RESULT 34**  
 US-10-282-122A-69408

**GENERAL INFORMATION:**

- APPLICANT: Wang, Liangsu
- APPLICANT: Zamudio, Carlos
- APPLICANT: Malone, Cheryl

**Query Match 83.9%; Score 47; DB 4; Length 323;**

**Best Local Similarity 88.9%; Pred. No. 19; Mismatches 0; Gaps 0;**

**Matches 8; Conservative 0; Indels 1;**

**Remaining Prior Application data removed - See File Wrapper or PALM.**

**NUMBER OF SEQ ID NOS: 78614**

**SOFTWARE: PatentIn version 3.1**

**SEQ ID NO: 67673**

**LENGTH: 323**

**TYPE: PRT**

**ORGANISM: Pseudomonas putida**

---

**RESULT 34**  
 US-10-282-122A-69408

**GENERAL INFORMATION:**

- APPLICANT: Wang, Liangsu
- APPLICANT: Zamudio, Carlos
- APPLICANT: Malone, Cheryl

**Query Match 83.9%; Score 47; DB 4; Length 323;**

**Best Local Similarity 88.9%; Pred. No. 19; Mismatches 0; Gaps 0;**

**Matches 8; Conservative 0; Indels 1;**

**Remaining Prior Application data removed - See File Wrapper or PALM.**

**NUMBER OF SEQ ID NOS: 78614**

**SOFTWARE: PatentIn version 3.1**

**SEQ ID NO: 67673**

**LENGTH: 323**

**TYPE: PRT**

**ORGANISM: Pseudomonas putida**

---

/ APPLICANT: OUYANG, HUI  
 / PINDER, BENJAMIN  
 / APPLICANT: RICHARDS, DAWN  
 / APPLICANT: TAI, MATTHEW  
 / APPLICANT: THALAKADA, ROSANNE  
 / APPLICANT: VALLEE, FRANCOIS  
 / APPLICANT: VITRAG, CRISTINA  
 / TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA  
 / FILE REFERENCE: ITP-205\_01  
 / CURRENT APPLICATION NUMBER: US/10/958,216  
 / CURRENT FILING DATE: 2004-10-04  
 / PRIOR APPLICATION NUMBER: PCT/CA03/00462  
 / PRIOR FILING DATE: 2003-04-02  
 / PRIOR APPLICATION NUMBER: 60/369,511  
 / PRIOR FILING DATE: 2002-04-02  
 / PRIOR APPLICATION NUMBER: 60/385,089  
 / PRIOR FILING DATE: 2002-05-31  
 / PRIOR APPLICATION NUMBER: 60/385,751  
 / PRIOR FILING DATE: 2002-06-04  
 / PRIOR APPLICATION NUMBER: 60/386,553  
 / PRIOR FILING DATE: 2002-06-05  
 / PRIOR APPLICATION NUMBER: 60/386,577  
 / PRIOR FILING DATE: 2002-06-05  
 / PRIOR APPLICATION NUMBER: 60/386,367  
 / PRIOR FILING DATE: 2002-06-05  
 / PRIOR APPLICATION NUMBER: 60/386,566  
 / PRIOR FILING DATE: 2002-06-05  
 / PRIOR APPLICATION NUMBER: 60/386,390  
 / PRIOR FILING DATE: 2002-06-06  
 / PRIOR APPLICATION NUMBER: 60/386,601  
 / PRIOR FILING DATE: 2002-06-06  
 / NUMBER OF SEQ ID NOS: 1132  
 / SOFTWARE: PatentIn Ver. 3.3  
 / SEQ ID NO: 469  
 / LENGTH: 55  
 / TYPE: PRT  
 / ORGANISM: Enterococcus faecalis  
 / US-10-958-216-469

Query Match 82.1%; Score 46; DB 5; Length 55;  
 Best Local Similarity 77.8%; Pred. No. 5.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALPPCH 9  
 Db 47 LAALPPCHA 55

**RESULT 37**  
 US-10-282-122A-57222  
 / Sequence 57222, Application US/10282122A  
 / Publication No. US20040029129A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Lianggu  
 / APPLICANT: Zamudio, Carlos  
 / APPLICANT: Malone, Cheryl  
 / APPLICANT: Haselbeck, Robert  
 / APPLICANT: Ohlsen, Kari  
 / APPLICANT: Zyskind, Judith  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John  
 / APPLICANT: Carr, Grant  
 / APPLICANT: Yamamoto, Robert  
 / APPLICANT: Forsyth, R.  
 / APPLICANT: Xu, H.  
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 / FILE REFERENCE: ELITRA 034A  
 / CURRENT APPLICATION NUMBER: US/10/282,122A  
 / CURRENT FILING DATE: 2003-02-20  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: 60/230,335  
 / PRIOR FILING DATE: 2000-09-06  
 / PRIOR APPLICATION NUMBER: 60/230,347  
 / PRIOR FILING DATE: 2000-09-09  
 / PRIOR APPLICATION NUMBER: 60/242,578  
 / PRIOR FILING DATE: 2000-10-23  
 / PRIOR APPLICATION NUMBER: 60/253,625  
 / PRIOR FILING DATE: 2000-11-27  
 / PRIOR APPLICATION NUMBER: 60/257,931  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: 60/267,636  
 / PRIOR FILING DATE: 2001-02-09  
 / SEQ ID NO: 57222  
 / LENGTH: 315  
 / TYPE: PRT  
 / ORGANISM: Enterococcus faecalis

**RESULT 38**  
 US-10-437-963-163320  
 / Sequence 163320, Application US/10437963  
 / Publication No. US2004012334A1  
 / GENERAL INFORMATION:  
 / APPLICANT: La Rosa, Thomas J.  
 / APPLICANT: Kovacic, David K.  
 / APPLICANT: Zhou, Yihua  
 / APPLICANT: Cao, Yongwei  
 / APPLICANT: Wu, Wei  
 / APPLICANT: Boukharov, Andrey A.  
 / APPLICANT: Barbazuk, Brad  
 / APPLICANT: Li, Bing  
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 / CURRENT APPLICATION NUMBER: US/10/437,963  
 / CURRENT FILING DATE: 2003-05-14  
 / NUMBER OF SEQ ID NOS: 204966  
 / SEQ ID NO: 163320  
 / LENGTH: 297  
 / TYPE: PRT  
 / ORGANISM: Oryza sativa  
 / FEATURE:

**RESULT 39**  
 US-10-958-216-464  
 / Sequence 192, Application US/10282122A  
 / Publication No. US20040029129A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Lianggu  
 / APPLICANT: Zamudio, Carlos  
 / APPLICANT: Malone, Cheryl  
 / APPLICANT: Haselbeck, Robert  
 / APPLICANT: Ohlsen, Kari  
 / APPLICANT: Zyskind, Judith  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John  
 / APPLICANT: Carr, Grant  
 / APPLICANT: Yamamoto, Robert  
 / APPLICANT: Forsyth, R.  
 / APPLICANT: Xu, H.  
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 / FILE REFERENCE: ELITRA 034A  
 / CURRENT APPLICATION NUMBER: US/10/282,122A  
 / CURRENT FILING DATE: 2003-02-20  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: 60/230,335  
 / PRIOR FILING DATE: 2000-09-06  
 / PRIOR APPLICATION NUMBER: 60/230,347  
 / PRIOR FILING DATE: 2000-09-09  
 / PRIOR APPLICATION NUMBER: 60/242,578  
 / PRIOR FILING DATE: 2000-10-23  
 / PRIOR APPLICATION NUMBER: 60/253,625  
 / PRIOR FILING DATE: 2000-11-27  
 / PRIOR APPLICATION NUMBER: 60/257,931  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: 60/267,636  
 / PRIOR FILING DATE: 2001-02-09  
 / SEQ ID NO: 57222  
 / LENGTH: 315  
 / TYPE: PRT  
 / ORGANISM: Enterococcus faecalis

**RESULT 40**  
 US-10-282-122A-57222  
 / Sequence 192, Application US/10282122A  
 / Publication No. US20040029129A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Lianggu  
 / APPLICANT: Zamudio, Carlos  
 / APPLICANT: Malone, Cheryl  
 / APPLICANT: Haselbeck, Robert  
 / APPLICANT: Ohlsen, Kari  
 / APPLICANT: Zyskind, Judith  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John  
 / APPLICANT: Carr, Grant  
 / APPLICANT: Yamamoto, Robert  
 / APPLICANT: Forsyth, R.  
 / APPLICANT: Xu, H.  
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 / FILE REFERENCE: ELITRA 034A  
 / CURRENT APPLICATION NUMBER: US/10/282,122A  
 / CURRENT FILING DATE: 2003-02-20  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: 60/230,335  
 / PRIOR FILING DATE: 2000-09-06  
 / PRIOR APPLICATION NUMBER: 60/230,347  
 / PRIOR FILING DATE: 2000-09-09  
 / PRIOR APPLICATION NUMBER: 60/242,578  
 / PRIOR FILING DATE: 2000-10-23  
 / PRIOR APPLICATION NUMBER: 60/253,625  
 / PRIOR FILING DATE: 2000-11-27  
 / PRIOR APPLICATION NUMBER: 60/257,931  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: 60/267,636  
 / PRIOR FILING DATE: 2001-02-09  
 / SEQ ID NO: 57222  
 / LENGTH: 315  
 / TYPE: PRT  
 / ORGANISM: Enterococcus faecalis

Sequence 464, Application US/10958216  
Publication No. US20050181388A1

GENERAL INFORMATION:  
 APPLICANT: EDWARDS, ALED  
 APPLICANT: DHARAMSINGH, AKIL  
 APPLICANT: VEDADI, MASOUD  
 APPLICANT: ALAM, MUHAMMAD ZAHOR  
 APPLICANT: ARROWSMITH, CHERYL E.  
 APPLICANT: BEATTIE, BRYAN  
 APPLICANT: BUZADZIJA, KRISTINA  
 APPLICANT: CANADIEN, VERONICA  
 APPLICANT: DOMAGALA, MEGAN  
 APPLICANT: HOUSTON, SIMON  
 APPLICANT: KANGARAJAH, DHUSHY  
 APPLICANT: LI, QIN  
 APPLICANT: MANSOURY, KAMRAN  
 APPLICANT: McDONALD, MERRY-LYNN  
 APPLICANT: NEHTERY, KATHLEEN  
 APPLICANT: NG, IVY  
 APPLICANT: PINDER, BENJAMIN  
 APPLICANT: RICHARDS, DAWN  
 APPLICANT: TAI, MATTHEW  
 APPLICANT: THALAKADA, ROSANNE  
 APPLICANT: VALLEE, FRANCOIS  
 APPLICANT: VIRAG, CRISTINA  
 TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA  
 FILE REFERENCE: IPT-205-01  
 CURRENT APPLICATION NUMBER: US/10/958,216  
 CURRENT FILING DATE: 2004-10-04  
 PRIOR APPLICATION NUMBER: PCT/CA03/00462  
 PRIOR FILING DATE: 2003-04-12  
 PRIOR APPLICATION NUMBER: 60/369,511  
 PRIOR FILING DATE: 2002-04-02  
 PRIOR APPLICATION NUMBER: 60/385,089  
 PRIOR FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: 60/385,751  
 PRIOR FILING DATE: 2002-06-14  
 PRIOR APPLICATION NUMBER: 60/386,553  
 PRIOR FILING DATE: 2002-06-05  
 PRIOR APPLICATION NUMBER: 60/386,577  
 PRIOR FILING DATE: 2002-06-05  
 PRIOR APPLICATION NUMBER: 60/386,367  
 PRIOR FILING DATE: 2002-06-05  
 PRIOR APPLICATION NUMBER: 60/386,566  
 PRIOR FILING DATE: 2002-06-05  
 PRIOR APPLICATION NUMBER: 60/386,390  
 PRIOR FILING DATE: 2002-06-06  
 PRIOR APPLICATION NUMBER: 60/386,601  
 PRIOR FILING DATE: 2002-06-06  
 Remaining Prior Application data removed - See File Wrapper or PAM.  
 NUMBER OF SEQ ID NOS: 1132  
 SEQ ID NO: 464  
 LENGTH: 315  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-10-958-216-464

Query Match 82.1%; Score 46; DB 5; Length 315;  
 Best Local Similarity 77.8%; Pred. No. 26; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 1; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 192 MALPPCSTM 200

RESULT 39  
 US-10-958-216-466

Query Match 82.1%; Score 46; DB 5; Length 315;  
 Best Local Similarity 77.8%; Pred. No. 26; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 1; Gaps 0;

Qy 2 MALPPCHAL 10  
 Db 192 MALPPCSTM 200

RESULT 40  
 US-10-282-122A-70335

Sequence 70335, Application US/10282122A  
 Publication No. US20040029129A1

GENERAL INFORMATION:  
 APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: EL/TRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 70335

LENGTH: 318

TYPE: PRT

ORGANISM: *Staphylococcus aureus*

US-10-282-122A-70335

Query Match Score 82.1%; DB 4; Length 318;

Best Local Similarity 77.8%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 196 MALPPCHTM 204

RESULT 41

US-10-282-122A-70576

General Information:

Sequence 70576, Application US/10282122A

Publication No. US/040029129A1

Query Match Score 82.1%; DB 4; Length 318;

Best Local Similarity 77.8%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 196 MALPPCHTM 204

RESULT 42

US-10-282-122A-70811

General Information:

Sequence 70811, Application US/10282122A

Publication No. US/040029129A1

General Information:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: EL/TRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

```

FEATURE;
NAME/KEY: MISS_FEATURE
LOCATION: (242) ; (242)
OTHER INFORMATION: X-any amino acid
US-10-282-122A-71845

Query Match 82.1%; Score 46; DB 4; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 196 MALPPCHTM 204

RESULT 44
US-10-857-625-654
; Sequence 654, Application US/10857625
; Publication No. US20050026189A1
GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; INVENTION: MICROBIAL OPERONS
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857-625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 654
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-857-625-654

Query Match 82.1%; Score 46; DB 5; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 196 MALPPCHTM 204

RESULT 45
US-09-855-604-277
; Sequence 277, Application US/09855604
; Publication No. US20040214165A1
GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSTING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,525
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Sphingylococcus haemolyticus
; SEQ ID NO 71845
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 277

```

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LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
us-09-855-604-277

Query Match    78.6%; Score 44; DB 3; Length 51;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0;
Gaps 0;
Qy      1 IMALPPCPH 10
Db      25 LVSLPPCPPL 34

RESULT 46
US-09-855-604-277
; Sequence 277, Application US/09855604
; Publication No. US20050158714A9
; GENERAL INFORMATION
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: DELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA, VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND PREVENTING TUBERCULOSIS
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03/15.0062-0100
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/1485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01613
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 277
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
us-09-855-604-277

Query Match    78.6%; Score 44; DB 3; Length 51;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0;
Gaps 0;
Qy      1 IMALPPCPH 10
Db      25 LVSLPPCPPL 34

RESULT 47
US-09-864-408A-6614
; Sequence 6614, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkess, Richard A.
; TITLE OF INVENTION: Human Polynucleotides and Polypeptides Encoded by Human Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/1206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 6614
; LENGTH: 93

RESULT 48
US-10-425-115-185774
; Sequence 185774, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
; FILE REFERENCE: 38-21(532)22(B)
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 185774
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(135)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_101012C_1.pep
; US-10-425-115-185774

Query Match    78.6%; Score 44; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0;
Indels 0;
Gaps 0;
Qy      2 MALPCH 8
Db      10 MALPCH 16

RESULT 49
US-09-867-550-396
; Sequence 396, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: Polynucleotides from Athrogenic Cells and Their Use
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US/N 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 396
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: wherein Xaa may be any one of Phe or Ser or Tyr or Cys or Leu or  
US-09-867-550-396

Query Match      78.6%;    Score 44;    DB 3;    Length 136;  
Best Local Similarity    77.8%;    Pred. No. 25;  
Matches    7;    Conservative    1;    Mismatches    1;    Indels    0;    Gaps    0;  
Qy            2 MALPPCHAL 10  
Db            55 VALPPCCTL 63

---

RESULT 50  
US-10-767-701-43390  
; Sequence 43390, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
;   APPLICANT: Kovacic, David K.  
;   APPLICANT: Zhou, Yihua  
;   APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(5353)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 43390  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C28633\_1.pep  
US-10-767-701-43390

Query Match      78.6%;    Score 44;    DB 4;    Length 148;  
Best Local Similarity    100.0%;    Pred. No. 27;  
Matches    7;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;  
Qy            2 MALPPCH 8  
Db            25 MALPPCH 31

Search completed: February 17, 2006, 02:48:20  
Job time : 183 secs